

Query Match	Score	DB 6	Length
100.0%	1547	1547	

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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LOCUS Sequence 1 from Patent WO0037613.

DEFINITION AX026529

ACCESSION AX026529.1 GI:10187717

VERSION AX026529.1 GI:10187717

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

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Query Match 100.0%; Score 1547; DB 6; Length 1547;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ACCESSION AJ245709
 VERSION AJ245709.1 GI:5804885
 KEYWORDS Akt-3; Akt3 gene.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
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 AUTHORS
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 JOURNAL
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ACCESSION	AF085234			
VERSION	AF085234.1 GI:17529662			
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SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			
REFERENCE	Li, X., Yu, L., Huang, H., Zhang, M., Zhao, Y., and Zhao, S.			
AUTHORS	Cloning of a novel human cDNA, STK-2, which encodes a rat			
TITLE	serine-threonine protein kinase (STK) homolog			
JOURNAL	Unpublished			
REFERENCE	Zhao, Y.			
AUTHORS	Direct Submission			
TITLE	Submitted (22-AUG-1998) Zhao Y., Institute of Genetics, Fudan			
JOURNAL	University, Lab of Human Gene Research, No. 220, Handan Road,			
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ORIGIN

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Query Match      100.0%; Score 1547; DB 9; Length 1706;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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LOCUS AF124141  
DEFINITION Homo sapiens protein kinase B gamma mRNA, complete cds.  
ACCESSION AF124141  
VERSION AF124141.1 GI:4757578  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE 1 (bases 1 to 1708)  
Brodebeck,D., Cron,P. and Hemmings,B.A.  
A human protein kinase Bgamma with regulatory phosphorylation sites  
in the activation loop and in the C-terminal hydrophobic domain  
JOURNAL 5. Biol. Chem. 274 (14), 9133-9136 (1999)  
MEDLINE 99194749  
PUBMED 10092583  
REFERENCE 2 (bases 1 to 1708)  
Brodebeck,D., Cron,P. and Hemmings,B.A.  
AUTHORS Direct Submission  
TITLE
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JOURNAL Submitted (27-JAN-1999) Friedrich Miescher-Institut,
Maulbeerallee 66, Basel 4058, Switzerland
FEATURES Location/Qualifiers
source 1.1708

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ORIGIN

Query Match 99.9%; Score 1545.4; DB 9; Length 1708;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1546; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 6
BD260777 2367 bp DNA linear PAR 17-JUL-2003
LOCUS BD260777
DEFINITION Human protein kinase B-gamma polypeptide and method of degrading
nonhuman protein kinase B-gamma.
ACCESSION BD260777
VERSION BD260777.1 GI:33070547
KEYWORDS JP 2002539823-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2367)

AUTHORS
TITLE
JOURNAL
COMMENT
Biovitrum AB
OS Homo sapiens (human)
PN JP 2002539823-A/1
PD 26-NOV-2002
PR 23-MAR-2000 JP 2000608727
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PC C12N9/12, C12Q1/48, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, PC
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PC G01N33/566, G01N33/573, C12N15/00, C12N5/00
CC active phosphorylation site
CC putative active phosphorylation site
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RESULT 7
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DEFINITION Homo sapiens AKT3 protein kinase mRNA, complete cds.
ACCESSION AF135794
VERSION AF135794.1 GI:4574743
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 1 (bases 1 to 2811)
 AUTHORS Nakatani, K., Sakaue, H., Thompson, D. A., Weigel, R. J., and Roth, R. A.
 TITLE Identification of a human Akt3 (protein kinase B gamma) which
 contains the regulatory serine phosphorylation site
 JOURNAL Biochem. Biophys. Res. Commun. 257 (3), 906-910 (1999)
 MEDLINE 9925329
 PUBMED 10208883
 REFERENCE 2 (bases 1 to 2811)
 AUTHORS Thompson, D. A., Nakatani, K., and Sakaue, H.
 TITLE Direct Submission
 JOURNAL Submitted (18-MAR-1999) Surgery, MSIS Building, Room P228, 1201
 Welch Road, Stanford, CA 94305, USA
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ORIGIN

Query Match 99.4%; Score 1537; DB 9; Length 2811;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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TITLE Method for controlling apoptosis and polypeptide controlling
JOURNAL Patient: WO 0215925-A 5 28-FEB-2002;
KYOMA HAKKO KOGYO CO LTD, TAKASHI TSURUO, NAOYA FUJITA, SAORI SATO
COMMENT OS Homo sapiens (human)
PN WO 0215925-A/5
PD 28-FEB-2002
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PI TAKASHI TSURUO, NAOYA FUJITA, SAORI SATO
PC A61K38/17, A61K38/45, A61K39/395, A61K45/00, A61P43/00, A61P3/08,
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ACCESSION AY335691
VERSION AY335691.1 GI:33304020
KEYWORDS FLI CDNA.
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Park, J., Rolfe, A., Hu, Y., Shen, B., Vamberg, F., Moreira, D.,
Kelley, T., Zuo, D., Raphael, J., Baqui, M., Jepson, D., Harlow, E.,
Labeier, J., and Britzuela, L.
Cloning of human full-length CDS FLK gene kinases in
recombinational vector system
Unpublished
2 (bases 1 to 1440)
Park, J., Rolfe, A., Hu, Y., Shen, B., Vamberg, F., Moreira, D.,

Kelley, T., Zuo, D., Raphael, J., Baqui, M., Jepson, D., Harlow, E.,
Labber, J. and Brizuela, L.
Direct Submission
Submitted (02-JUL-2003) Biological Chemistry and Molecular
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,
Cambridge, MA 02141-2023, USA

COMMENT

This CDS clone is a part of a collection of human full-length
expression clones generated by Harvard Institute of Proteomics.
Each CDS has been cloned without stop-codon (to allow fusion with
C-terminal tag). The CDS has been directionally cloned using BD
In-Fusion(TM) cloning system between the SalI and HindIII sites of
the pDNR-Dual vector. Additional sequences in the clone: 'Acc'
after SalI site and before 'Atg' to provide Kozak consensus
sequence; 'GG' after last codon and before HindIII site to maintain
reading frame.

FEATURES

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gene

CDS

ORIGIN

Query Match 93.0%; Score 1438; DB 12; Length 1440;
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Matches 1438; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION BD251227 GI:33060997
VERSION JP 2002535964-A/2.
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SOURCE Homo sapiens
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1436)
AUTHORS Masure, S.L.J. and Richardson, A.
TITLE Human Akt-3
JOURNAL Patent: JP 2002535964-A 2 29-OCT-2002;
JANSSEN PHARMACEUTICA NV
COMMENT OS Homo sapiens (human)
PN JP 2002535964-A/2
PD 29-OCT-2002
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DEFINITION Sequence 2 from Patent WO0037613.
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 Patent: WO 0037613-A 2-29-JUN-2000;
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RESULT 13
 BD250154 1570 bp DNA linear PAT 17-JUL-2003
 LOCUS AKT nucleic acids, polypeptides, and uses thereof.
 DEFINITION BD250154
 ACCESSION BD250154.1 GI:33059924
 VERSION JP 2002539781-A/1.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1570)
 Guo, K., Pagnoni, M.F., Clark, K.L. and Ivaashchenko, Y.D.
 AKT nucleic acids, polypeptides, and uses thereof
 Patent: JP 2002539781-A 1 26-NOV-2002;
 AVENTIS PHARMACEUTICALS PRODUCTS INC
 OS Homo sapiens (human)
 PN JP 2002539781-A/1
 PD 26-NOV-2002
 PF 14-MAR-2000 JP 2000606725
 PI 19-MAR-1999 US 60/125108
 P1 KUN GUO, MARCO F PAGNONI, KENNETH L CLARK, YURI D IVASHCHENKO PC
 C12N15/09, A61K9/127, A61K35/76, A61K38/00, A61K39/395, A61K47/36, PC
 A61K47/42,

PC A61K47/46,A61K48/00,A61P1/16,A61P9/10,A61P13/12,A61P37/06, PC
A61P43/00,
PC C07K16/40,C12N1/19,C12N1/21,C12N5/10,C12N7/00,C12N9/12,C12Q1/
PC 48,G01N33/15,
G01N33/50,G01N33/53,G01N33/56/(C12N1/19,C12R1:645),(C12N1/21, PC
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ORIGIN

Query Match 88.2%; Score 1364.8; DB 6; Length 1570;
Best Local Similarity 98.4%; Pred. No. 1.3e-297;
Matches 1378; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

1 GGGAGTCATCATGAGCGATGTTACATTTGTGAAAAGAGGTTGGCTTCAGAAAGGGGAGA 60
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61 AAT 120
176 AAT 235
121 AAT 180
236 AAT 295
181 AAT 240
296 AAT 355
241 CCAAGTGCATCTGTTATATAGAGAACATTTGATGATGATCTCCAGAGAAAGGAGAGA 300
356 CCAAGTGCATCTGTTATATAGAGAACATTTGATGATGATCTCCAGAGAAAGGAGAGA 415
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416 ATGACAGAGAGCTATCCAGGCTGTAGACAGACTGCAGAGGCAAGAGAGAGAGAT 475
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716 CAGAGAT 775
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1081 AAT 1140
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LOCUS Sequence 1 from Patent WO0077190.
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ACCESSION AX056819
VERSION
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SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
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Guo,K., Ivashchenko,Y. and Clark,K.
Induction of vascular endothelial growth factor (vegf) by the
serine/threonine protein kinase akt
Patent: WO 0077190-A 1 21-DEC-2000;
JOURNAL
Aventis Pharmaceuticals Inc. (US)
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ORIGIN

Query Match 88.2%; Score 1364.8; DB 6; Length 1570;
Best Local Similarity 98.4%; Pred. No. 1.3e-287;
Matches 1378; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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DB 836 GTGAGAGAGCGGGGTGTTCTCTGAGAGACCGCACAGCTTTCTATGTCAGAAAATGTCTC 895
QY 781 TGCCCTTGAGTATCTACATTTCCGGAAGATTTGTGTACCGTGATCTCAAGTTGGAAGATCT 840
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RESULT 15
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 Guo, K., Pagnoni, M.F., Clark, K.L. and Ivashchenko, Y. D.
Akt nuclear acids, polypeptides, and uses thereof
Patent: WO 0168850-A 1 20-SEP-2001;
Aventis Pharmaceuticals Products Inc. (US)
Location/Qualifiers

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ORIGIN

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Query Match 88.2%; Score 1364.8; DB 6; Length 1570;
Best Local Similarity 98.4%; Pred. No. 1.3e-297;
Matches 1378; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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Search completed: April 13, 2005, 06:12:26
Job time : 6629 secs

XX Claim 3: Fig 1: 61bp; English.

CC The present sequence encodes human Akt-3. Akt-3 is a third human isoform
 CC of Akt, which is also known as protein kinase B (PKB) or "related to A
 CC and C protein kinase" (RAC-PK). The gene encoding "Akt-3" is located on
 CC human chromosome 1, region q43-q44. A human hippocampal EST sequence that
 CC showed high similarity to the rat RAC-PKgamma sequence was used to design
 CC primers for 3' rapid amplification of cDNA ends (3' RACE). The sequence
 CC obtained in the first round of 3' RACE was used to design primers for a
 CC second round. The complete sequence was then amplified from human
 CC hippocampal cDNA by PCR using primers based on the product of the second
 CC round of 3' RACE. Akt can inhibit apoptosis induced by detachment from
 CC the extracellular matrix. The Akt-3 nucleic acid molecule and protein may
 CC be used as medicaments for treating cancer. Agents which influence the
 CC activity of Akt-3 protein, and so stimulate apoptosis, may also be used
 CC to treat diseases associated with Akt-3

XX Sequence 1547 BP; 515 A; 276 C; 348 G; 408 T; 0 U; 0 Other;

Query Match 100.0%; Score 1547; DB 3; Length 1547;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

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DB 721 GTGAG 780
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RESULT 2
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 XX ADN71939;
 XX
 XX 12-AUG-2004 (first entry)
 XX
 DE Human serine/threonine kinase Akt-3 encoding cDNA SEQ ID NO:25.
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 XX kinase pathway inhibitor; anti-prostate cancer;
 XX mitogen-activated protein kinase pathway inhibitor;
 KW MAP kinase pathway inhibitor; prostate cancer inhibitor;
 KW phosphatidylinositol 3-kinase/Akt kinase pathway;
 KW PI3K/Akt kinase pathway; cytoskeletal; MAP kinase inhibitor;
 KW phosphatidylinositol 3-kinase/Akt kinase inhibitor;
 KW PI3K/Akt kinase inhibitor; androgen receptor inhibitor; prostate cancer;

KW human; serine/threonine kinase Akt-3; chromosome 1; gene; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
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 FT /product= "serine/threonine kinase Akt-3"
 PN WO2004041185-A2.
 XX
 XX 21-MAY-2004.
 PD
 XX
 PF 31-OCT-2003; 2003WO-US034636.
 XX
 PR 31-OCT-2002; 2002US-0423340P.
 XX
 PA (UVRP) UNIV ROCHESTER.
 XX
 PI Chang C, Lee Y, Lin W;
 DR WPI; 2004-390508/36.
 DR P-PSDB; ADN71940.
 XX
 PT Composition useful in the treatment of e.g. prostate cancer comprises a
 PT kinase pathway inhibitor and an anti-prostate cancer compound.
 XX
 PS Disclosure; SEQ ID NO 25; 118bp; English.
 XX
 CC The present invention describes a composition (C1) which comprises a
 CC kinase pathway inhibitor (a) and an anti-prostate cancer compound (b).
 CC Also described: (1) identification of a mitogen-activated protein (MAP)
 CC kinase pathway inhibitor involving incubating an androgen or a
 CC library of molecules with a cell containing an activable MAP kinase
 CC pathway and selecting the molecules which inhibit the activation of the
 CC MAP kinase pathway; and (2) identification of a prostate cancer inhibitor
 CC involving incubating a cell with hydroxyflutamide and potential
 CC inhibitor, and assaying the level of activation of MAP kinase pathway or
 CC phosphatidylinositol 3-kinase (PI3K)/Akt kinase pathway. C1 has
 CC cytostatic activity, and can be used as a MAP kinase inhibitor.
 CC phosphatidylinositol 3-kinase (PI3K)/Akt kinase inhibitor, and androgen
 CC receptor (AR) inhibitor. C1 can be used in the treatment of prostate
 CC cancer; for identifying a MAP kinase pathway inhibitor; for identifying a
 CC prostate cancer inhibitor; and for reducing the number of prostate cancer
 CC cells in a sample. The composition C1 provides effective combination
 CC therapy as compared to prior therapies. The present sequence encodes
 CC human serine/threonine kinase Akt-3, which is used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 1547 BP; 515 A; 276 C; 348 G; 408 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1547; DB 12; Length 1547;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 241 CCAAGTGAAGTCTGTTATAGAGAAACATTTGATGATGATCTCCAGAGAAAGGAGAGA 300
 QY
 Db 301 ATGACAGAAAGCTATTCAGGCTGTGACAGACGACTGACAGAGCAAGAAAGAGAGAT 360
 QY
 Db 301 ATGACAGAAAGCTATTCAGGCTGTGACAGACGACTGACAGAGCAAGAAAGAGAGAT 360
 QY
 Db 361 GAATGTAGTCCAACTTCAAAATGATTAATAGAGAGAGAGATGATGCTCTAC 420
 QY
 Db 361 GAATGTAGTCCAACTTCAAAATGATTAATAGAGAGAGAGATGATGCTCTAC 420
 QY
 Db 421 AACCCATCAATAAAGAAAGACATGATGATTTGATTAATTTGAACTACTAGTAAAG 480
 QY
 Db 421 AACCCATCAATAAAGAAAGACATGATGATTTGATTAATTTGAACTACTAGTAAAG 480
 QY
 Db 481 CACTTTGGGAAAGTTATTTGGTTGACAGAGAAAGCAAGTGGAAATATATGCTATGAA 540
 QY
 Db 481 CACTTTGGGAAAGTTATTTGGTTGACAGAGAAAGCAAGTGGAAATATATGCTATGAA 540
 QY
 Db 541 GATTCGAAAGAAAGATGATTTGACAAAGATGAGAGAGCACTCTAAGTGAAG 600
 QY
 Db 541 GATTCGAAAGAAAGATGATTTGACAAAGATGAGAGAGCACTCTAAGTGAAG 600
 QY
 Db 601 CAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCCTTGAATATTCCTCCAGAC 660
 QY
 Db 601 CAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCCTTGAATATTCCTCCAGAC 660
 QY
 Db 661 AAAAGACGTTGTGTTTGTGATGAGATATGTTAATGGGGGAGCTGTTTCCATT 720
 QY
 Db 661 AAAAGACGTTGTGTTTGTGATGAGATATGTTAATGGGGGAGCTGTTTCCATT 720
 QY
 Db 721 GTGAGAGAGCGGGGTGTTCTGAGGACCGCACAGTTTCTAATGGGAGAAATGTC 780
 QY
 Db 721 GTGAGAGAGCGGGGTGTTCTGAGGACCGCACAGTTTCTAATGGGAGAAATGTC 780
 QY
 Db 781 TGCCTTGAAGTATCTACATTTCCGAAAGATGTGATCCGTGATCTCAAGTTGAGAGATCT 840
 QY
 Db 781 TGCCTTGAAGTATCTACATTTCCGAAAGATGTGATCCGTGATCTCAAGTTGAGAGATCT 840
 QY
 Db 841 AATGCTGACAAAGATGCGCACATTAATAATTCAGATTTTGAATTTGCAAAAGAGGAT 900
 QY
 Db 841 AATGCTGACAAAGATGCGCACATTAATAATTCAGATTTTGAATTTGCAAAAGAGGAT 900
 QY
 Db 901 CACAGATGAGGACACATGAGAAACATTCGTGAGCACTCCAGAAATCTGGACACAGAGT 960
 QY
 Db 901 CACAGATGAGGACACATGAGAAACATTCGTGAGCACTCCAGAAATCTGGACACAGAGT 960
 QY
 Db 961 GTTAGAAGATTAATGACTATGCGGAGAGATGAGTGTGGGCTTAGAGGTTGTCAATGA 1020
 QY
 Db 961 GTTAGAAGATTAATGACTATGCGGAGAGATGAGTGTGGGCTTAGAGGTTGTCAATGA 1020
 QY
 Db 1021 TGAATGATGTGTGGAGGTTACCTTTCTACACACAGACCAATGAGAACTTTTGAAT 1080
 QY
 Db 1021 TGAATGATGTGTGGAGGTTACCTTTCTACACACAGACCAATGAGAACTTTTGAAT 1080
 QY
 Db 1081 AATATTAATGAGAAACATTAATTTCTGGAACACTCTTCAAGATGCAAAATCATTTGCT 1140
 QY
 Db 1081 AATATTAATGAGAAACATTAATTTCTGGAACACTCTTCAAGATGCAAAATCATTTGCT 1140
 QY
 Db 1141 TTCAGGCTCTTGATTAAGATTCCTTCTGAGTAACTGGCAAGATGTATATGATTAATA 1200
 QY
 Db 1141 TTCAGGCTCTTGATTAAGATTCCTTCTGAGTAACTGGCAAGATGTATATGATTAATA 1200
 QY
 Db 1201 AGAAATTAAGACACAGTTTCTTCTGAGTAACTGGCAAGATGTATATGATTAATA 1260
 QY
 Db 1201 AGAAATTAAGACACAGTTTCTTCTGAGTAACTGGCAAGATGTATATGATTAATA 1260
 QY
 Db 1261 GCTTGTAAGTCTTTTAAACCTCAAGTAACTGTAAGACAGATCTAGATATTTTGAATGA 1320
 QY
 Db 1261 GCTTGTAAGTCTTTTAAACCTCAAGTAACTGTAAGACAGATCTAGATATTTTGAATGA 1320
 QY
 Db 1321 AGAATTTACAGCTCAGACTATTAACAATTAACAACCTGAAATATATGATGAGATGTAT 1380
 QY
 Db 1321 AGAATTTACAGCTCAGACTATTAACAATTAACAACCTGAAATATATGATGAGATGTAT 1380

QY 1381 GGAGTCATGACATGAGAGGCGCGGATTTCCCTCAATTTTCTACTGCAAGTGG 1440
 CC |||||
 Db 1381 GGAGTCATGACATGAGAGGCGCGGATTTCCCTCAATTTTCTACTGCAAGTGG 1440
 QY 1441 ACGAGATAAGTCTCTTTCATTTCTGCTACTGCTCATCTTCATTTATTACTGAAA 1500
 CC |||||
 Db 1441 ACGAGATAAGTCTCTTTCATTTCTGCTACTGCTCATCTTCATTTATTACTGAAA 1500
 QY 1501 TGAATTCCTGGAGATCCAGCTCTTACTCTTACACTTACAGGGGGA 1547
 CC |||||
 Db 1501 TGAATTCCTGGAGATCCAGCTCTTACTCTTACACTTACAGGGGGA 1547
 RESULT 3
 AAC77341
 ID AAC77341 standard; cDNA, 3285 BP.
 XX AAC77341;
 AC AAC77341;
 DT 08-FEB-2001 (first entry)
 XX
 DE Human ORF2896 polynucleotide sequence SEQ ID NO:5791.
 XX
 XX Human; open reading frame; ORF; detection; cytosolic; hepatotropic;
 KW vulnery; antiproliferative; antiparkinsonian; neurotropic; neuroprotective;
 KW anticonvulsant; osteopathic; antirheumatic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antineoplastic;
 KW antiviral; antibacterial; antifungal; antirheumatic; antihypertensive;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antineoplastic disease; coagulation;
 KW thrombosis; contraceptive; ss.
 XX
 OS Homo sapiens.
 XX
 XX MO200058473-A2.
 XX
 PD 05-OCT-2000.
 XX
 PF 31-MAR-2000; 2000MO-US008621.
 XX
 XX 31-MAR-1999; 99US-0127607P.
 PR 02-APR-1999; 99US-0127636P.
 PR 05-APR-1999; 99US-0127728P.
 PR 30-MAR-2000; 2000US-00540763.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 PI Shimkete RA, Leach M;
 XX
 DR WPI: 2000-602362/57.
 DR P-PSDB: AAB43132.
 XX
 PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease.
 XX
 PS Claim 5; Page 4956-4958; 5507pp; English.
 XX
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORF open reading frames 1 to 3161. The ORF
 CC sequences have activities such as: cytosolic; hepatotropic; vulnery;
 CC antiproliferative; antiparkinsonian; neurotropic; neuroprotective; osteopathic;
 CC anticonvulsant; antirheumatic; immunosuppressant; immunostimulant;
 CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
 CC dermatological; immunosuppressive; antineoplastic; antibacterial;
 CC antiviral; antifungal; antirheumatic; antihypertensive; antianemic. The

CC sequences can be used for determining the presence of or predisposition
 CC to, or preventing or treating pathological conditions associated with an
 CC ORF-associated disorder. The nucleic acids can be used to express ORF
 CC proteins in gene therapy vectors. The proteins and nucleic acids may be
 CC used to treat cancers, proliferative disorders, neurodegenerative
 CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
 CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
 CC storage, systemic lupus erythematosus, severe combined immunodeficiency
 CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
 CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
 CC cartilage damage, nocturnal haemoglobinuria, antineoplastic disease; to
 CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
 CC
 XX
 SQ Sequence 3285 BP; 1028 A; 624 C; 690 G; 942 T; 0 U; 1 Other;
 Query Match 99.9%; Score 1545.4; DB 3; Length 3285;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1546; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGAGTCATGACATGAGAGGCGCGGATTTCCCTCAATTTTCTACTGCAAGTGG 60
 Db 465 GGAGTCATGACATGAGAGGCGCGGATTTCCCTCAATTTTCTACTGCAAGTGG 524
 QY 61 ATATATATAAACTGGAGCGCAAGATCTCTTTTGAAGACAGATGCTCATTAAG 120
 Db 525 ATATATATAAACTGGAGCGCAAGATCTCTTTTGAAGACAGATGCTCATTAAG 584
 QY 121 ATATATAAGAAAGCTCAAGATGATGATTTACTTATCCCTCAACATTTTCAGTGG 180
 Db 585 ATATATAAGAAAGCTCAAGATGATGATTTACTTATCCCTCAACATTTTCAGTGG 644
 QY 181 AAAATGCCAGTTAATGAAAAGCAAGACCAAGCAACATTTATATATAGATGCT 240
 Db 645 AAAATGCCAGTTAATGAAAAGCAAGACCAAGCAACATTTATATATAGATGCT 704
 QY 241 CCAAGTGAATCTGTTATGAGAGAACTTTATGATGATGATCTCCAGAGAAAGGAAAG 300
 Db 705 CCAAGTGAATCTGTTATGAGAGAACTTTATGATGATGATCTCCAGAGAAAGGAAAG 764
 QY 301 ATGACAGAAAGTATCCAGCGCTGTAGCAGACAGATGAGAGGCAAGAAAGAGAGANT 360
 Db 765 ATGACAGAAAGTATCCAGCGCTGTAGCAGACAGATGAGAGGCAAGAAAGAGAGANT 824
 QY 361 GAATGTAGTCCAACTTCAAAATGATATATATAGAGAGAGATGATGCTCTTAC 420
 Db 825 GAATGTAGTCCAACTTCAAAATGATATATATAGAGAGAGATGATGCTCTTAC 884
 QY 421 AACCATATATAAAGAAAGCAATGATGATTTTGAATTTTGAATTTTGAATTTTGA 480
 Db 885 AACCATATATAAAGAAAGCAATGATGATTTTGAATTTTGAATTTTGAATTTTGA 944
 QY 481 CACTTTGGGAAAGTATTTTGTTCGAGAGAGGCAAGTGAATTTTGAATTTTGA 540
 Db 945 CACTTTGGGAAAGTATTTTGTTCGAGAGAGGCAAGTGAATTTTGAATTTTGA 1004
 QY 541 GATTTGAAAGAAAGAGTATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 600
 Db 1005 GATTTGAAAGAAAGAGTATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 1064
 QY 601 CAGATATTAAGAAAGTATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 660
 Db 1065 CAGATATTAAGAAAGTATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 1124
 QY 661 AAAAAGCCGTTTGTGTTTGTGATGAGATTTTGAATTTTGAATTTTGAATTTTGA 720
 Db 1125 AAAAAGCCGTTTGTGTTTGTGATGAGATTTTGAATTTTGAATTTTGAATTTTGA 1184
 QY 721 GTTCGAGAGAGGAGTCTCTGAGAGCGGACAGCTTTCTATGATGAGAAATTTGCTC 780
 Db 1185 GTTCGAGAGAGGAGTCTCTGAGAGCGGACAGCTTTCTATGATGAGAAATTTGCTC 1244
 QY 781 TGCCTTGAGACTATCTACATTCGAGAAAGATTTGATCCGTGATCTCAAGTTGAGAAATCT 840

Db	1245	TGCCTTGACATATCTACACTTCGCGAAGAATTGTGTACCGTGTATCTCAAGTTGGAGATCT	1304
Qy	841	AATGCTGGACAAAGATGGCCCATTAATAAATTTACAGATTTTGGACTTTGGCAAGAAGGAT	900
Db	1305	AATGCTGGACAAAGATGGCCCATTAATAAATTTACAGATTTTGGACTTTGGCAAGAAGGAT	1364
Qy	901	CACAGATTCAGCCACCATGAAAGACATTCTGTGGCCTCCAGAAATCTTGGCACCAGAGT	960
Db	1365	CACAGATTCAGCCACCATGAAAGACATTCTGTGGCCTCCAGAAATCTTGGCACCAGAGT	1424
Qy	961	GTTGGAATATATGACTATGGCCGAGAGTGTGACTGTGGGGGCGTAGGGGTTGTCACTA	1020
Db	1425	GTTGGAATATATGACTATGGCCGAGAGTGTGACTGTGGGGGCGTAGGGGTTGTCACTA	1484
Qy	1021	TGAATATGATGTGTGGAGGTTACCTTTCTCAACACGAGCACCATGAGAACTTTTGAATT	1080
Db	1485	TGAATATGATGTGTGGAGGTTACCTTTCTCAACACGAGCACCATGAGAACTTTTGAATT	1544
Qy	1081	AATATTAATGGAAGACATTAATTTCTTCGAACTCTTTCAGATGCAAAATCATTTGCT	1140
Db	1545	AATATTAATGGAAGACATTAATTTCTTCGAACTCTTTCAGATGCAAAATCATTTGCT	1604
Qy	1141	TTTCAGGGGCTCTTGATAAAGATCCAAATAAAGCCTTGTGTGAGGACCAAGATGATGCAA	1200
Db	1605	TTTCAGGGGCTCTTGATAAAGATCCAAATAAAGCCTTGTGTGAGGACCAAGATGATGCAA	1664
Qy	1201	AGAAATTTATGAGACACAGTTTCTTCTCTGAGATTAATCGGCAGATGTATATGATTAATA	1260
Db	1665	AGAAATTTATGAGACACAGTTTCTTCTCTGAGATTAATCGGCAGATGTATATGATTAATA	1724
Qy	1261	GCTTGTACCTCTCTTTAAACCTCAAGTAACCTTGAGACAGATATCTAGATATTTTGATGA	1320
Db	1725	GCTTGTACCTCTCTTTAAACCTCAAGTAACCTTGAGACAGATATCTAGATATTTTGATGA	1784
Qy	1321	AGAAATTTACACTCAGACTATTTACAATAACACACTGTAATAAATATGATGAGATGTAT	1380
Db	1785	AGAAATTTACACTCAGACTATTTACAATAACACACTGTAATAAATATGATGAGATGTAT	1844
Qy	1381	GGACTGCATGACAAATGAGAGGCGCGCCGATTTCCCTCAATTTTCTCTACTCTGCAAGTGG	1440
Db	1845	GGACTGCATGACAAATGAGAGGCGCGCCGATTTCCCTCAATTTTCTCTACTCTGCAAGTGG	1904
Qy	1441	ACGAGAAATTAAGTCTCTTTCAATTCGTCTCACTTCACGTATCTTCAATTTATTAAGTAAA	1500
Db	1905	ACGAGAAATTAAGTCTCTTTCAATTCGTCTCACTTCACGTATCTTCAATTTATTAAGTAAA	1964
Qy	1501	TGATTTCTTGACATACCAAGTCTTACGTCTTTACACATATGCAAGGGGCA	1547
Db	1965	TGATTTCTTGACATACCAAGTCTTACGTCTTTACACATATGCAAGGGGCA	2011
RESULT 4			
ACC61592	AAC61592 standard; DNA; 2367 BP.		
XX	XX	AAC61592;	
XX	XX	19-FEB-2001 (first entry)	
XX	XX	DNA encoding a human kinase B-gamma polypeptide.	
XX	XX	Human; protein kinase B gamma; PKB; insulin; insulin growth factor 1;	
KV	KV	phosphoinositide 3-kinase; insulin signaling;	
KW	KW	pleckstrin homology domain; ss.	
XX	XX	Homo sapiens.	
OS	XX		
FH	XX	Key	Location/Qualifiers
FT	XX	CDS	10..1449
FT	XX		/*tag= a
FT	XX		/product= "kinase B-gamma polypeptide"
PN	XX	WO200058446-A1.	

XX	05-OCT-2000.
XX	23-MAR-2000; 2000OWO-SE000571.
XX	25-MAR-1999; 99SE-00001115.
XX	(PHAA) PHARMACIA & UPJOHN AB.
XX	Atersand A;
XX	WPI; 2000-647230/62.
XX	P-PSDB; AAB19284.
XX	Novel human protein kinase B gamma polynucleotides and polypeptides
XX	PT useful as probe or primers in polymerase chain reaction and to raise
XX	PT antibodies useful in diagnostic assays for detecting polypeptide
XX	expression.
XX	Claim 1; Page 16-19; 27p; English.
XX	The present sequence encodes a human protein kinase B gamma (PKB)
XX	polypeptide. PKB is activated by insulin or insulin growth factor 1.
XX	lipid products of phosphoinositide 3-kinase act in insulin signalling by
XX	binding to pleckstrin homology domains of PKB. PKB polynucleotides may be
XX	used as a source of probes and primers. PKB polypeptides are used to
XX	raise antibodies, which are used in diagnostic assays. The polypeptides
XX	are also useful for screening for compounds which affect insulin
XX	signalling pathways
XX	Sequence 2367 BP; 752 A; 444 C; 514 G; 657 T; 0 U; 0 Other;
XX	Query Match 99.8%; Score 1544.4; DB 3; Length 2367;
XX	Best Local Similarity 99.9%; Pred. No. 0;
XX	Matches 1545; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY	2 GGAGTCATCATGAGCGATGTTACCATTTGTGAAAGAGGTGGTTGAGAAAGGGAGAA 61
DB	1 GGAGTCATCATGAGCGATGTTACCATTTGTGAAAGAGGTGGTTGAGAAAGGGAGAA 60
QY	62 TATATATAAACTGGAAGCCCAAGTACTCTTTTGAAGACAGATGGCTCATTTAGAGA 121
DB	61 TATATATAAACTGGAAGCCCAAGTACTCTTTTGAAGACAGATGGCTCATTTAGAGA 120
QY	122 TATAAAGAAAGCACTCAAGATGTGTGATTTACCTTATCCCTCAACATTTTCAGTGGCA 181
DB	121 TATAAAGAAAGCACTCAAGATGTGTGATTTACCTTATCCCTCAACATTTTCAGTGGCA 180
QY	182 AAATGCCAGTTATGATAAAGCAAGACGAACCAAGCCAAACATTTATATCAGATGCTC 241
DB	181 AAATGCCAGTTATGATAAAGCAAGACGAACCAAGCCAAACATTTATATCAGATGCTC 240
QY	242 CAGTGGACTACTGTTATAGAGAAACATTTATGATGATCTCCAGAGAAAGGAGAGA 301
DB	241 CAGTGGACTACTGTTATAGAGAAACATTTATGATGATCTCCAGAGAAAGGAGAGA 300
QY	302 TGGACAGAGGATTCACAGGCTGTGACGACAGATCGACAGAGCAAGAGAGAGAGATG 361
DB	301 TGGACAGAGGATTCACAGGCTGTGACGACAGATCGACAGAGCAAGAGAGAGAGATG 360
QY	362 AATTGTAGTCCAACTTCACAATTTGATATATAGAGAGAGAGATGATGCTTACA 421
DB	361 AATTGTAGTCCAACTTCACAATTTGATATATAGAGAGAGAGATGATGCTTACA 420
QY	422 ACCCATCTAATAAGAAAGCAATGATGATTTGACTATTTGAAACTATAGTAAAGGC 481
DB	421 ACCCATCTAATAAGAAAGCAATGATGATTTGACTATTTGAAACTATAGTAAAGGC 480
QY	482 ACTTTGGGAAGTATTTTGGTTCGAGAGAGCAAGTGGAAATCTATAGCTATGAG 541
DB	481 ACTTTGGGAAGTATTTTGGTTCGAGAGAGCAAGTGGAAATCTATAGCTATGAG 540
QY	542 ATTCTGAAGAAGAAGTCATATTTGCAAGAGATGAAGTGCGACACCTTAATCGAAGC 601

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Db      541 ATTCTGAAGAAAGAGTCATTAATGCAAGATGAAGTGGACACACTCTAATCTGAAAGC 600
Qy      602 AAGATTTAAAGAAACCTAGACATCCCTTTTAAACATCCTTAAATATCTCTCCAGACA 661
Db      601 AAGATTTAAAGAAACCTAGACATCCCTTTTAAACATCCTTAAATATCTCTCCAGACA 660
Qy      662 AAAGACCGTTTGTGTTTGTGATGAAATGTTAAATGGGGGAGCGTGTTCATTTG 721
Db      661 AAAGACCGTTTGTGTTTGTGATGAAATGTTAAATGGGGGAGCGTGTTCATTTG 720
Qy      722 TCGAAGAGCGGGGTGTTCTCTGAGAGCGCGACACGTTTCTATGTGACAGAAATGTCTCT 781
Db      721 TCGAAGAGCGGGGTGTTCTCTGAGAGCGCGACACGTTTCTATGTGACAGAAATGTCTCT 780
Qy      782 GCGTTGACATCTCATCTCCGAGAAAGATGTGTACCGGATCTCAAGTGGAGATCTCA 841
Db      781 GCGTTGACATCTCATCTCCGAGAAAGATGTGTACCGGATCTCAAGTGGAGATCTCA 840
Qy      842 ATGCTGACAAAGATGCGCCACATATAAATTAAGATTTTGAATTGGCAAGAGGATC 901
Db      841 ATGCTGACAAAGATGCGCCACATATAAATTAAGATTTTGAATTGGCAAGAGGATC 900
Qy      902 ACAGATGACGCCACCATGAAAGACATTTGTGSCACTCCAGAAATATCTGSCACCAAGATG 961
Db      901 ACAGATGACGCCACCATGAAAGACATTTGTGSCACTCCAGAAATATCTGSCACCAAGATG 960
Qy      962 TTAGAAGATTAATGACATATGCGGAGACATGAGTGTGGGCTGAGGGTTCATGAT 1021
Db      961 TTAGAAGATTAATGACATATGCGGAGACATGAGTGTGGGCTGAGGGTTCATGAT 1020
Qy      1022 GAATGATGTGTGGAGGTTACCTTCTCAACACGAGACCATGAGAACTTTTGAATTA 1081
Db      1021 GAATGATGTGTGGAGGTTACCTTCTCAACACGAGACCATGAGAACTTTTGAATTA 1080
Qy      1082 AATTTAATGAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTTCTT 1141
Db      1081 AATTTAATGAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTTCTT 1140
Qy      1142 TCAGGGCTCTTGAATTAAGATCAAAATTAACGCTTGTGGAGGACCAATGATGCAAAA 1201
Db      1141 TCAGGGCTCTTGAATTAAGATCAAAATTAACGCTTGTGGAGGACCAATGATGCAAAA 1200
Qy      1202 GAATTTATGAGACACAGTTTCTCTCTGAGATTAATCTGCAAGATGATATATAAAG 1261
Db      1201 GAATTTATGAGACACAGTTTCTCTCTGAGATTAATCTGCAAGATGATATATAAAG 1260
Qy      1262 CTGTGACCTCTTTTAAACCTCAAGTACATCTGAGACAGATTAATGATATTTGATGA 1321
Db      1261 CTGTGACCTCTTTTAAACCTCAAGTACATCTGAGACAGATTAATGATATTTGATGA 1320
Qy      1322 GAATTTAAGCTCAAGCTTTCATTAATTAACACCACTGAAATTAATGATGATG 1381
Db      1321 GAATTTAAGCTCAAGCTTTCATTAATTAACACCACTGAAATTAATGATGATG 1380
Qy      1382 GATCATGAGACATGAGAGGCGCGCATTTCCCTCAATTTTCTACTCTGCAAGTGA 1441
Db      1381 GATCATGAGACATGAGAGGCGCGCATTTCCCTCAATTTTCTACTCTGCAAGTGA 1440
Qy      1442 CGAGAAATTAAGTCTCTTTCATCTGCTACTCTGCTCACTGTCATCTTCAATTTA 1501
Db      1441 CGAGAAATTAAGTCTCTTTCATCTGCTACTCTGCTCACTGTCATCTTCAATTTA 1500
Qy      1502 GATTCCTGAGACATCAACCACTCTAGCTCTTAACATAGAGAGGGGCA 1547
Db      1501 GATTCCTGAGACATCAACCACTCTAGCTCTTAACATAGAGAGGGGCA 1546

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RESULT 5
ADCC26888
ID ADCC26888 standard; DNA; 2811 BP.
XX
AC ADCC26888;

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XX      18-DEC-2003 (first entry)
DT      DNA encoding human Akt3.
XX
DE      de; gene; Akt; human; apoptosis; myocardial infarction;
XX      hyperproliferative disease; cancer; rheumatoid arthritis;
XX      inflammatory bowel disease; osteoarthritis; leiomyoma; adenoma; lipoma;
XX      haemangioma; fibroma; vascular occlusion; restenosis; atherosclerosis;
XX      pre-neoplastic lesion; adenomatous hyperplasia;
XX      prostatic intraepithelial neoplasia; carcinoma in situ;
XX      oral hairy leukoplakia; psoriasis.
XX
OS      Homo sapiens.
XX
PN      US2003144204-A1.
XX
PD      31-JUL-2003.
XX
PF      19-DEC-2002; 2002US-00324985.
XX
PR      19-DEC-2001; 2001US-0342155P.
XX
PA      (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI      Spencer D;
XX
PT      WPI; 2003-720709/68.
XX
PS      New expression vector for modulating apoptosis or for treating myocardial
XX      infarction or cancer, comprises an inducible chimeric protein that
XX      comprises a mutant Akt polypeptide fused to a ligand-binding domain.
XX
XX      Disclosure; SEQ ID NO 4; 38bp; English.
XX
CC      The invention relates to an expression vector comprising an inducible
CC      chimeric protein in which a mutant Akt polypeptide fused to a
CC      ligand-binding domain. The composition and methods are useful in
CC      modulating apoptosis or in treating myocardial infarction or
CC      hyperproliferative diseases such as cancer, rheumatoid arthritis,
CC      inflammatory bowel disease, osteoarthritis, leiomyoma, adenoma,
CC      lipoma, haemangiomas, fibromas, vascular occlusion, restenosis,
CC      atherosclerosis, pre-neoplastic lesions (e.g. adenomatous hyperplasia or
CC      prostatic intraepithelial neoplasia), carcinoma in situ, oral hairy
CC      leukoplakia or psoriasis. The present sequence represents DNA encoding
CC      human Akt3.
XX
SQ      Sequence 2811 BP; 905 A; 506 C; 582 G; 818 T; 0 U; 0 Other;
XX
Query Match      99.4%; Score 1537; DB 10; Length 2811;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      11 ATGACGATGTTACCATTTGTGAAGAGTTGGTTCAAGAGGGGCAATATATAA 70
Db      1 ATGACGATGTTACCATTTGTGAAGAGTTGGTTCAAGAGGGGCAATATATAA 60
Qy      71 AACTGAGGCCCAAGTACTCTCTTTGAAGACAGATGCTCATTTATGATATTAAG 130
Db      61 AACTGAGGCCCAAGTACTCTCTTTGAAGACAGATGCTCATTTATGATATTAAG 120
Qy      131 AAACTCAAGATGTTGATTTTACCTTATCCCTCAACAATTTTCTAGTGGCAAAATGCCAG 190
Db      121 AAACTCAAGATGTTGATTTTACCTTATCCCTCAACAATTTTCTAGTGGCAAAATGCCAG 180
Qy      191 TTAATGAAGAACGAAACGACCAAGCCAAACATTTATATGATGTTCTCCAGTGA 250
Db      181 TTAATGAAGAACGAAACGACCAAGCCAAACATTTATATGATGTTCTCCAGTGA 240
Qy      251 ACTGTTATAGAGAGAACTTTTCAATGATATCTCCAGAGGAAAGGAATGACAGAA 310
Db      241 ACTGTTATAGAGAGAACTTTTCAATGATATCTCCAGAGGAAAGGAATGACAGAA 300

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QY	311	GCTATCCAGGCTGTGCGAGCAGACTCGACAGGCGAAGAAAGAGAGATGAATTTGATG	370
Db	301	GCTATCCAGGCTGTGCGAGCAGACTCGAGAGGCGAAGAGAGAGATGAATTTGATG	360
QY	371	CCAACTTCACAAATTGATATATATAGAGAGGAAGATGGAATGCCCTCAACCCATCAT	430
Db	361	CCAACTTCACAAATTGATATATATAGAGAGGAAGATGGAATGCCCTCAACCCATCAT	420
QY	431	AAAAAAGACAAATGAATTTGACTATTTGAACTACTAGTAAAGGCACTTTTGGG	490
Db	421	AAAAAAGACAAATGAATTTGACTATTTGAACTACTAGTAAAGGCACTTTTGGG	480
QY	491	AAAGTTATTTGGTTCGAGAGAGGCGAAGTGAATAATCTATGCTATGAAGATTCGAAG	550
Db	481	AAAGTTATTTGGTTCGAGAGAGGCGAAGTGAATAATCTATGCTATGAAGATTCGAAG	540
QY	551	AAAGAAGCATTAATTGCAAAAGATGAAGTGAAGCAGCTCTAATCTGAAGAAGAGATATA	610
Db	541	AAAGAAGCATTAATTGCAAAAGATGAAGTGAAGCAGCTCTAATCTGAAGAAGAGATATA	600
QY	611	AAGAACACTAGACATCCCTTTTAAACATCTTGAATATATCCCTTCAGACAAAAGACCGT	670
Db	601	AAGAACACTAGACATCCCTTTTAAACATCTTGAATATATCCCTTCAGACAAAAGACCGT	660
QY	671	TTGTGTTTGTGATGGAATATGTTAATGAGGCGAGCTGTTTTCCATTTGTCGAGAG	730
Db	661	TTGTGTTTGTGATGGAATATGTTAATGAGGCGAGCTGTTTTCCATTTGTCGAGAG	720
QY	731	CGGGTGTTCTCGAGAGCCGCAACGTTTTCTATGATGCAAGAAATGTCTCTGCTTGGAC	790
Db	721	CGGGTGTTCTCGAGAGCCGCAACGTTTTCTATGATGCAAGAAATGTCTCTGCTTGGAC	780
QY	791	TATCTACATTCGCGAAAAGATTGTATACCGTGATCTCAAGTTGAGAACTATATGCTGGAC	850
Db	781	TATCTACATTCGCGAAAAGATTGTATACCGTGATCTCAAGTTGAGAACTATATGCTGGAC	840
QY	851	AAAGATGGCCACATAAAAATTACAGATTTTGACTTTGCCAAAGAGGATCACAGATGCA	910
Db	841	AAAGATGGCCACATAAAAATTACAGATTTTGACTTTGCCAAAGAGGATCACAGATGCA	900
QY	911	GGCACCATGAAAGCAATTCTGTGGCACTCCAAATATCTGGCACGAGAGTGTAGAAAT	970
Db	901	GGCACCATGAAAGCAATTCTGTGGCACTCCAAATATCTGGCACGAGAGTGTAGAAAT	960
QY	971	AATGACTATGGCGGAGCAGTAGACTGTGGGGGCGTAAGGGGTTGTCAATATGAAGATGATG	1030
Db	961	AATGACTATGGCGGAGCAGTAGACTGTGGGGGCGTAAGGGGTTGTCAATATGAAGATGATG	1020
QY	1031	TGTGGGAGGTTACCTTTTCTACAAACGAGACCAATGAAACTTTTGAATTAATTAATG	1090
Db	1021	TGTGGGAGGTTACCTTTTCTACAAACGAGACCAATGAAACTTTTGAATTAATTAATG	1080
QY	1091	GAAAGCATTAATTTTCTCGAACACTCTCTTCAGATGCAAAATCAATTGCTTCAGGGCTC	1150
Db	1081	GAAAGCATTAATTTTCTCGAACACTCTCTTCAGATGCAAAATCAATTGCTTCAGGGCTC	1140
QY	1151	TTGATTAAGAGATCCAAATTAAGCGCTGTGGAGAGACAGATGATGCAAAAAGAAATATG	1210
Db	1141	TTGATTAAGAGATCCAAATTAAGCGCTGTGGAGAGACAGATGATGCAAAAAGAAATATG	1200
QY	1211	AGACAAGTTTCTTCTCGAGTAATCTGGCAAGATGTAATGATTAAGAAAGCTTGTAACCT	1270
Db	1201	AGACAAGTTTCTTCTCGAGTAATCTGGCAAGATGTAATGATTAAGAAAGCTTGTAACCT	1260
QY	1271	CGTTTTAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTTGAAGAAATTTTACA	1330
Db	1261	CGTTTTAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTTGAAGAAATTTTACA	1320
QY	1331	GCTCAGACTATTAACAATACACACACTGAAAAAATGATGAGAGATGATGACCTGACATG	1390
Db	1321	GCTCAGACTATTAACAATACACACACTGAAAAAATGATGAGAGATGATGACCTGACATG	1380
QY	1391	GACAAATGAGAGCGGCGCATTTCCCTCAATTTTCTTCACTCTGCAAGTGAAGAGAAATA	1450

Db	1381	GACAAATAGAGGGCGCGCAATTTCCCAATTTTCTCACTGCAAGTGAACGAAATAA	1440
Qy	1451	GTCTCTTCAATTCGTCTACTTCACTGTCATCTTCAATTTATTACTGAAATGATTCCTGG	1510
Db	1441	GTCTCTTTCATTCTGCTACTTCACTGTCATCTTCAATTTATTACTGAAATGATTCCTGG	1500
Qy	1511	ACATCACCAGTCTAGCTTTCACATGACATGACAGGGGCA	1547
Db	1501	ACATCACCAGTCTAGCTTTCACATGACATGACAGGGGCA	1537
RESULT 6			
ADQ88265			
ID	ADQ88265	standard; DNA; 2811 BP.	
XX	ADQ88265;		
AC			
XX			
DT	21-OCT-2004	(first entry)	
XX			
DE	Human	14180 DNA encodes a rac gamma Ser/Thr protein kinase RAC-PK-gamma.	
XX			
KW	human; gene; ds; cardiovascular disorder; thrombotic disorder;		
KW	differential expression; gene therapy; aberrant vasculatiation;		
KW	atherosclerosis; thromboisis; coronary artery disease; hyperlipidaemia;		
KW	dyslipidaemia; high blood pressure; heart failure; cardiatic;		
KW	thrombolytic; anticoagulant; antilipaeamic; hypotensive; cardiatic;		
XX	rac gamma Ser/Thr protein kinase; RAC-PK-gamma.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2004063340-A2.		
XX			
PD	29-JUL-2004.		
XX			
FP	13-JAN-2004;	2004WO-US000393.	
XX			
PR	13-JAN-2003;	2003US-0439683P.	
PR	05-FEB-2003;	2003US-0445216P.	
PR	18-FEB-2003;	2003US-0448036P.	
PR	12-MAR-2003;	2003US-0454189P.	
PR	25-MAR-2003;	2003US-0457541P.	
PR	29-APR-2003;	2003US-0460411P.	
PR	08-MAY-2003;	2003US-0469041P.	
PR	10-JUN-2003;	2003US-0477414P.	
PR	13-JUN-2003;	2003US-0478560P.	
PR	24-JUL-2003;	2003US-0489772P.	
PR	28-JUL-2003;	2003US-0490660P.	
PR	03-SEP-2003;	2003US-0498938P.	
PR	22-SEP-2003;	2003US-0504786P.	
PR	24-SEP-2003;	2003US-0505570P.	
PR	17-OCT-2003;	2003US-0512418P.	
PR	27-OCT-2003;	2003US-0514660P.	
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Stagliano NE, Healy A, Acton SL, Galvin KM, Donoghue MA;		
PI	Rogrigue-Way A, Tomlinson JE;		
XX			
DR	WPI; 2004-553729/53.		
DR	P-PSDB; ADQ88266.		
XX			
PT	Identifying a compound for treating a cardiovascular or thrombotic		
PT	disorder by combining a compound to be tested with e.g., a 9380, 9462,		
PT	8701 or 2419 polypeptide or with a host cell expressing the polypeptide		
PT	and detecting the binding.		
XX			
PS	Claim 1; SEQ ID NO 107; 512pp; English.		
XX			
CC	This invention relates to a novel compound that is capable of treating a		
CC	cardiovascular or thrombotic disorder. Specifically, it refers to the		
CC	identification of nucleic acid molecules, and the encoded proteins		
CC	thereof, which are differentially expressed in cardiovascular disease		

CC states relative to their normal expression in non-diseased tissue. The
 CC present invention describes test compounds (i.e. small molecules,
 CC peptides or antibodies) that can bind to and modulate the activity of
 CC these differentially expressed membrane-bound polypeptides, where binding
 CC is detected by a competition binding assay, immunoassay or yeast two-
 CC hybrid assay. Accordingly, pharmaceutical compositions can be developed
 CC and used via gene therapy to treat aberrant vascularisation,
 CC atherosclerosis, thrombosis, coronary artery disease, hyperlipidemia,
 CC dyslipidemia, high blood pressure or heart failure. As such, they
 CC exhibit cardiant, chromolytic, anticoagulant, antilipemic, hypotensive
 CC and cardiant activities. This polynucleotide sequence is a human DNA
 CC molecule that is differentially expressed in a patient with a
 CC cardiovascular disorder, given in an exemplification of the invention.

XX Sequence 2811 BP; 905 A; 506 C; 582 G; 818 T; 0 U; 0 Other;

Query Match 99.4%; Score 1537; DB 13; Length 2811;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ATGAGCGATGTTACCATGTGAAAGAGGTTGGGTTCAAGAGGGGAGATATATATAA 70
 Db 1 ATGAGCGATGTTACCATGTGAAAGAGGTTGGGTTCAAGAGGGGAGATATATATAA 60
 QY 71 AACTGAGGCCAAGATCTCTTTTGAAGACAGATGCTCATCTTCAATGATATATAAG 130
 Db 61 AACTGAGGCCAAGATCTCTTTTGAAGACAGATGCTCATCTTCAATGATATATAAG 120
 QY 131 AAACCTCAAGATGATGATTTTACCTTATCCCTCAACAATCTTTCACTGCGAAATGCCAG 190
 Db 121 AAACCTCAAGATGATGATTTTACCTTATCCCTCAACAATCTTTCACTGCGAAATGCCAG 180
 QY 191 TTATGAAACAGACAGACCAAGCAACATTTATATATAGATGTCCTCAGTGGACT 250
 Db 181 TTATGAAACAGACAGACCAAGCAACATTTATATATAGATGTCCTCAGTGGACT 240
 QY 251 ACTGTTATAGAGAACATTTCTATGATATCTCAAGAGAAAGGAGATATGACAGAA 310
 Db 241 ACTGTTATAGAGAACATTTCTATGATATCTCAAGAGAAAGGAGATATGACAGAA 300
 QY 311 GCTATTCAGGCTGTAGCAGACCTGCAAGGCAAGAAAGAGAGATGATTTAGT 370
 Db 301 GCTATTCAGGCTGTAGCAGACCTGCAAGGCAAGAAAGAGAGATGATTTAGT 360
 QY 371 CCAACTTCACAATTTATATATAGAGAGAAAGATGATGCTCTCAACCCATCAT 430
 Db 361 CCAACTTCACAATTTATATATAGAGAGAAAGATGATGCTCTCAACCCATCAT 420
 QY 431 AAAAGAAAGACATGATGATTTTGAATTTGAAATCTAAGTAAAGGCACTTTTGGG 490
 Db 421 AAAAGAAAGACATGATGATTTTGAATTTGAAATCTAAGTAAAGGCACTTTTGGG 480
 QY 491 AAAAGTATTTTGGTTGAGAGAAAGGCAAGTGGAAAAATCTATGCTATGAAATTCGAG 550
 Db 481 AAAAGTATTTTGGTTGAGAGAAAGGCAAGTGGAAAAATCTATGCTATGAAATTCGAG 540
 QY 551 AAAAGAGTCATTTATTCAGAGATGAAGTGGCAACACTCTAATCTGAAAGCAGATATTA 610
 Db 541 AAAAGAGTCATTTATTCAGAGATGAAGTGGCAACACTCTAATCTGAAAGCAGATATTA 600
 QY 611 AAGAACATAGACATCCCTTTTAAACATCCTTGAAATATCTCTTCAGACAAAGACCGT 670
 Db 601 AAGAACATAGACATCCCTTTTAAACATCCTTGAAATATCTCTTCAGACAAAGACCGT 660
 QY 671 TTGTGTTTGTGATGAAATATGTTAATGGGGGCGAGCTGTTTTCATTTGTCGAGAGG 730
 Db 661 TTGTGTTTGTGATGAAATATGTTAATGGGGGCGAGCTGTTTTCATTTGTCGAGAGG 720
 QY 731 CGGGTGTCTCGAGAGACCGACAGCTTTCTAATGTCGAGAAATGTCCTGCTGGAG 790
 Db 721 CGGGTGTCTCGAGAGACCGACAGCTTTCTAATGTCGAGAAATGTCCTGCTGGAG 780
 QY 791 TATCTACATTCGGAAGATGTTGTATCGGTGATCTCAAGTTGAGAAATCTAAATGCTGAC 850

Db 781 TATCTACATTCGGAAGATGTTGTATCGGTGATCTCAAGTTGAGAAATCTAAATGCTGAC 840
 QY 851 AAAAGTGGCCATATAAAATTTACATATTTTGAATCTTTGCAAAAGAGATCAATATGA 910
 Db 841 AAAAGTGGCCATATAAAATTTACATATTTTGAATCTTTGCAAAAGAGATCAATATGA 900
 QY 911 GCCACCATGAGACATCTGTGTGGCACTCCAGAAATATCTGGCACAGAGGTGTGAAGAT 970
 Db 901 GCCACCATGAGACATCTGTGTGGCACTCCAGAAATATCTGGCACAGAGGTGTGAAGAT 960
 QY 971 AATGACTATGCGGAGCAGATGACTGTGGGGCTTGAAGGCTTGCATGTATGAAATGATG 1030
 Db 961 AATGACTATGCGGAGCAGATGACTGTGGGGCTTGAAGGCTTGCATGTATGAAATGATG 1020
 QY 1031 TGTGGAGGTTACCTTTCTACAAACAGACCAATGAAACCTTTGAAATTAATTAATG 1090
 Db 1021 TGTGGAGGTTACCTTTCTACAAACAGACCAATGAAACCTTTGAAATTAATTAATG 1080
 QY 1091 GAAGACATTTAATTTCTTCGAACACTCTCTTCAGATGCAAAATCATTCCTTTCAGGGCTC 1150
 Db 1081 GAAGACATTTAATTTCTTCGAACACTCTCTTCAGATGCAAAATCATTCCTTTCAGGGCTC 1140
 QY 1151 TTGATPAAAGATCCAAATPAAACGCTTGTGTGAGAGACCAATGATGCAAAAGAAATATG 1210
 Db 1141 TTGATPAAAGATCCAAATPAAACGCTTGTGTGAGAGACCAATGATGCAAAAGAAATATG 1200
 QY 1211 AGACACAGTTCTTCTCGAGATTAACGCGAAGATGATATGATPAAAGCTTCTACCT 1270
 Db 1201 AGACACAGTTCTTCTCGAGATTAACGCGAAGATGATATGATPAAAGCTTCTACCT 1260
 QY 1271 CTTTAAACCTCAAGTAACTGTGACAGATCTAGATATTTTGAAGAAATTTACA 1330
 Db 1261 CTTTAAACCTCAAGTAACTGTGACAGATCTAGATATTTTGAAGAAATTTACA 1320
 QY 1331 GCTCAGACTTATTACAATAACACACCTGAAAATATGATGAGATGATGACCTGCATG 1390
 Db 1321 GCTCAGACTTATTACAATAACACACCTGAAAATATGATGAGATGATGACCTGCATG 1380
 QY 1391 GACAAATGAGAGGCGGCGCATTTCCCTCAATTTCTCTCTCGCAAGTGGACAGAAATPA 1450
 Db 1381 GACAAATGAGAGGCGGCGCATTTCCCTCAATTTCTCTCTCGCAAGTGGACAGAAATPA 1440
 QY 1451 GTCTCTTCAATCTCTCACTTCACTGTCATCTTCAATTTATCTGAATGATTTCTGG 1510
 Db 1441 GTCTCTTCAATCTCTCACTTCACTGTCATCTTCAATTTATCTGAATGATTTCTGG 1500
 QY 1511 ACATCAACAGTCTAGCTTTACATAGACAGGGGCA 1547
 Db 1501 ACATCAACAGTCTAGCTTTACATAGACAGGGGCA 1537

RESULT 7
 AA62451
 ID AA62451 standard; cDNA; 1440 BP.
 XX
 XX AAA62451;
 DT 13-NOV-2000 (first entry)
 XX
 XX Human Akt-3 coding sequence.
 XX
 XX Human; Akt-3; protein kinase B; PKB; serine/threonine kinase; cytosolic;
 KW apoptosis stimulator; cancer; rapid amplification of cDNA ends; RACE;
 KW chromosome 1q43-44; 88.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1440
 FT /*tag= a
 FT /product= "Akt-3"
 XX

XX 20-JUN-2002 (first entry)
 XX Human Akt3 encoding cDNA SEQ ID NO:10.
 DE Human Akt3 encoding cDNA SEQ ID NO:10.
 XX Human; Hsp90 beta; Hsp90 alpha; Akt1; Akt2; Akt3; apoptosis regulation;
 KW apoptosis; serine/threonine kinase; heat shock protein; anticancer;
 KW cytosolic; cardiant; vasotropic; hepatotropic; neuroprotective;
 KW antidiabetic; neurotrophic; cancer; diabetes; Alzheimer's disease;
 KW cell death; radiation; brain ischaemia; cardiac ischaemia; gene; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..1440
 FT /tag= a
 FT /product= "Akt3"
 XX WO200215925-A1.
 XX 28-FEB-2002.
 XX 22-AUG-2001; 2001WO-UP007179.
 XX 22-AUG-2000; 2000JP-00251529.
 XX (KYOW) KYOMA HAKKO KOGYO KK.
 XX (TSURU/) TSURUO T.
 XX Tsuruo T, Fujita N, Sato S;
 DR WPI; 2002-292035/33.
 DR P-PSDB; ABB06998.
 PT Regulation of apoptosis by promoting or inhibiting the intracellular
 PT binding of Akt with Hsp90, useful for prevention and treatment of
 PT apoptosis-regulation associated diseases including cancer.
 XX Disclosure; Page 87-89; 93pp; Japanese.
 XX The present invention describes the regulation of apoptosis, in which the
 CC intracellular binding of Akt (a serine/threonine kinase) with Hsp90 (a
 CC heat-shock protein) is promoted or inhibited. The present invention also
 CC describes: (1) isoforms of Akt and Hsp90, and their partial peptides
 CC including the binding domain; (2) antibodies to Akt or Hsp90; (3) DNA
 CC encoding Akt or Hsp90 or their partial peptides including the binding
 CC domain; (4) expression vectors containing the DNA; (5) host cells
 CC transformed by the vectors; (6) production of Akt or Hsp90 or their
 CC partial peptides including the binding domain by culture of the
 CC transformed cells; (7) screening compounds for their ability to modify
 CC intracellular Akt activity by contact with cells expressing Akt or Hsp90;
 CC and (8) drug compositions containing antibodies recognizing the binding
 CC domain of Akt or Hsp90 and optionally also an anticancer agent. Akt and
 CC Hsp90 have cytosolic, cardiant, vasotropic, hepatotropic, antidiabetic,
 CC neuroprotective and neurotrophic activities. Blockade of the binding of
 CC Hsp90 with Akt increases the sensitivity of cells to apoptosis induction.
 CC Akt and Hsp90 can be used in the prevention and treatment of diseases
 CC with which apoptosis regulation is associated, including cancer (such as
 CC gastric cancer, ovarian cancer, breast cancer, pancreatic cancer and
 CC prostate cancer), diabetes, Alzheimer's disease, cell death caused by
 CC radiation or anticancer agents, brain ischaemia or cardiac ischaemia. The
 CC present sequence encodes human Akt3 which is used in the exemplification
 CC of the present invention
 XX
 SO Sequence 1440 BP; 489 A; 248 C; 330 G; 373 T; 0 U; 0 Other;
 Query Match 93.1%; Score 1440; DB 6; Length 1440;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1440; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 AACTGAGGCCAAGATACCTTCTTTGAAGACAGATGCTCATATAGATATAAAG 130
 DB 61 AACTGAGGCCAAGATACCTTCTTTGAAGACAGATGCTCATATAGATATAAAG 120
 QY 131 AAACCTCAAGATGTGGATTTTACCTTATCCCTCAACAATTTCAGTGGCAAAATGCCAG 190
 DB 121 AAACCTCAAGATGTGGATTTTACCTTATCCCTCAACAATTTCAGTGGCAAAATGCCAG 180
 QY 191 TTAATGAAAACGAAGCAACCAAGCCAAACATTTATATAGATGTCTCCAGTGGACT 250
 DB 181 TTAATGAAAACGAAGCAACCAAGCCAAACATTTATATAGATGTCTCCAGTGGACT 240
 QY 251 ACTGTTATAGAGAGAACTTTCATGTAGATATCCAGAGAGAAAGGAATATGACAGAA 310
 DB 241 ACTGTTATAGAGAGAACTTTCATGTAGATATCCAGAGAGAAAGGAATATGACAGAA 300
 QY 311 GCTATCCAGGCTGTAGCAGACAGACTGCAGAGGCAAGAAAGAGAGAAATGATTTGAT 370
 DB 301 GCTATCCAGGCTGTAGCAGACAGACTGCAGAGGCAAGAAAGAGAGAAATGATTTGAT 360
 QY 371 CCAACTTCACAAATTTGATATATATAGAGAGAGAAAGATGAGATGCTCTACAAACCATCAT 430
 DB 361 CCAACTTCACAAATTTGATATATATAGAGAGAGAAAGATGAGATGCTCTACAAACCATCAT 420
 QY 431 AAAAGAAAACAATGATGATTTTGTACTATTTGAAGTAACTAGTAAAGGCACTTTTGGG 490
 DB 421 AAAAGAAAACAATGATGATTTTGTACTATTTGAAGTAACTAGTAAAGGCACTTTTGGG 480
 QY 491 AAAGTTATTTGGTTCGAGAGAGGCAAGTGGAAAATATCTATGTATGAAATTTGTGAG 550
 DB 481 AAAGTTATTTGGTTCGAGAGAGGCAAGTGGAAAATATCTATGTATGAAATTTGTGAG 540
 QY 551 AAAGAGCATATATTTGCAAGAGATGAGGACACCTCTACGAAAGCAAGATATTA 610
 DB 541 AAAGAGCATATATTTGCAAGAGATGAGGACACCTCTACGAAAGCAAGATATTA 600
 QY 611 AAGAACAATGACATCCCTTTTAAACATCCCTTGAATATTTCTTCAGACAAAGACCGT 670
 DB 601 AAGAACAATGACATCCCTTTTAAACATCCCTTGAATATTTCTTCAGACAAAGACCGT 660
 QY 671 TTGTGTTTGTGATGATGATATGATATGAGGCGAGCTGTTTTCATTTGTGAGAGAG 730
 DB 661 TTGTGTTTGTGATGATGATATGATATGAGGCGAGCTGTTTTCATTTGTGAGAGAG 720
 QY 731 CGGATGTTCTCGAAGACCGCACAGTTTCTATGTGTGAGAAATGTCTCTGCTGAGC 790
 DB 721 CGGATGTTCTCGAAGACCGCACAGTTTCTATGTGTGAGAAATGTCTCTGCTGAGC 780
 QY 791 TATCTACATTCGGAAGAGATGTTGTACGATCTCAAGTTGAGAAATCTAATGCTGAGC 850
 DB 781 TATCTACATTCGGAAGAGATGTTGTACGATCTCAAGTTGAGAAATCTAATGCTGAGC 840
 QY 851 AAAGATGGCCACATATAAATTTACAGATTTTGGACTTTGCAAGAAAGGATCAAGATGCA 910
 DB 841 AAAGATGGCCACATATAAATTTACAGATTTTGGACTTTGCAAGAAAGGATCAAGATGCA 900
 QY 911 GCCACATGAAAGACATTTCTGTGGCACTCCAGAAATCTGGCACCGAGGTGTTAGAAAT 970
 DB 901 GCCACATGAAAGACATTTCTGTGGCACTCCAGAAATCTGGCACCGAGGTGTTAGAAAT 960
 QY 971 AATGACTATGCGCCGAGCAGTATGATGTGGGCTCAGAGGCTGTATGATGAAATGATG 1030
 DB 961 AATGACTATGCGCCGAGCAGTATGATGTGGGCTCAGAGGCTGTATGATGAAATGATG 1020
 QY 1031 TGTGGAGGTTACCTTTCTTACCAACGAGACCATGAGAAATCTTTGAAATTAATTAATG 1090
 DB 1021 TGTGGAGGTTACCTTTCTTACCAACGAGACCATGAGAAATCTTTGAAATTAATTAATG 1080
 QY 1091 GAAAGCATTAATTTTCTCTCGAACACTCTTCAAGATGCAAAATCAATGTCTTCAAGGCTC 1150
 DB 1081 GAAAGCATTAATTTTCTCTCGAACACTCTTCAAGATGCAAAATCAATGTCTTCAAGGCTC 1140

QY 1151 TTGATAAGAGATCCAAATAAACCCCTTGAGAGACAGATGATGCATAAAGAAATATG 1210
 |||||
 DB 1141 TTGATTAAGATTCCTAAATTAACCCCTTGAGAGACAGATGATGCATAAAGAAATATG 1200
 |||||
 QY 1211 AGACACAGTTCTTCTCTGAGTAACTGGCAAGATGATATGATAAAGCTTGTACCT 1270
 |||||
 DB 1201 AGACACAGTTCTTCTCTGAGTAACTGGCAAGATGATATGATAAAGCTTGTACCT 1260
 |||||
 QY 1271 CCTTTAAACCTCAAGTAATCTGAGACAGATCTAGATATTTTGTATGAAGATTTACA 1330
 |||||
 DB 1261 CCTTTAAACCTCAAGTAATCTGAGACAGATCTAGATATTTTGTATGAAGATTTACA 1320
 |||||
 QY 1331 GCTCAGACTTATCAATTAACCAACCTGAAATATGATGAGATGGTATGACTGATG 1390
 |||||
 DB 1321 GCTCAGACTTATCAATTAACCAACCTGAAATATGATGAGATGGTATGACTGATG 1380
 |||||
 QY 1391 GACAAATGAGAGGCGCGCATTTCCCTCAATTTTCTACTCTGCAAGTGGACGAGATA 1450
 |||||
 DB 1381 GACAAATGAGAGGCGCGCATTTCCCTCAATTTTCTACTCTGCAAGTGGACGAGATA 1440
 |||||

RESULT 9
 AAA96637
 ID AAA96637 standard; DNA; 1570 BP.
 XX
 AC AAA96637;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE DNA encoding a human Akt3 polypeptide.
 XX
 KM Human: Akt3; apoptotic cell death; apoptotic stimulating kinase 1; ASK1;
 KM hypoxia; apoptosis; necrosis; myocardial infarction; ischemia;
 KM reperfusion injury; myocardial ischemia reperfusion injury; stroke;
 KM liver damage; renal failure; organ transplantation; coronary artery; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 126..1523
 FT /*tag= a
 FT /product= "Akt3"
 XX
 PN MO200056866-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 14-MAR-2000; 2000MO-US006574.
 XX
 PR 19-MAR-1999; 99US-0125108P.
 XX
 PA (AVET) AVENTIS PHARM PROD INC.
 XX
 PI Guo K, Pagnoni MF, Clark KL, Ivashchenko YD;
 XX
 DR MPI: 2000-638260/61.
 XX
 DR P-PSDB; AABI9011.
 XX
 PT Novel AKT3 nucleic acid and proteins capable of preventing apoptotic cell
 PT death induced by apoptosis stimulating kinase 1 useful for treating
 PT myocardial infarction or ischemia reperfusion injury.
 XX
 PS Claim 3; Page 62-64; 73pp; English.
 XX
 CC The present sequence encodes a human Akt3 protein. Expression of Akt3
 CC prevents apoptotic cell death induced by apoptotic stimulating kinase 1
 CC (ASK1). The Akt3 polypeptide is useful for inhibiting cell death,
 CC preferably in a cardiac myocyte, resulting from hypoxia, apoptosis or
 CC necrosis in a patient suffering from myocardial infarction or ischemia
 CC reperfusion injury. The polypeptide is also useful for treating
 CC myocardial infarction or ischemia reperfusion injury, where the
 CC reperfusion injury is myocardial ischemia reperfusion injury or is
 CC associated with stroke, liver damage, renal failure, organ

CC transplantation or coronary artery by pass grafting
 XX
 SQ Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;
 Query Match 88.2%; Score 1364.8; DB 3; Length 1570;
 Best Local Similarity 98.4%; Pred. No. 0;
 Matches 1378; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 GGGAGTCATCATGAGGAGTTCACCTTTGTGAAGAAAGGTGGGTTCAAGAGGGGAGA 60
 |||||
 DB 116 GGGAGTCATCATGAGGAGTTCACCTTTGTGAAGAAAGGTGGGTTCAAGAGGGGAGA 175
 |||||
 QY 61 ATATATAAAGAACTGGAGGCGCAAGATACCTCTTTGAAGACAGATGGCTCATTAAG 120
 |||||
 DB 176 ATATATAAAGAACTGGAGGCGCAAGATACCTCTTTGAAGACAGATGGCTCATTAAG 235
 |||||
 QY 121 ATATAAAGAAACCTCAAGATGTGATTTACCTTATCCCTCAACAATTTTCACTGGC 180
 |||||
 DB 236 ATATAAAGAAACCTCAAGATGTGATTTACCTTATCCCTCAACAATTTTCACTGGC 295
 |||||
 QY 181 AAAATGCCAGTTATATGAAAAACAGACCAAGCCAAACACATTTATATCATATGCT 240
 |||||
 DB 296 AAAATGCCAGTTATATGAAAAACAGACCAAGCCAAACACATTTATATCATATGCT 355
 |||||
 QY 241 CCAGTGACACTAGTTATAGAGAAACATTCATGTAGATACCTCCAGAGAAAGGAGA 300
 |||||
 DB 356 CCAGTGACACTAGTTATAGAGAAACATTCATGTAGATACCTCCAGAGAAAGGAGA 415
 |||||
 QY 301 ATGACAGAAAGCTATCCAGGCTGTAGACAGACAGACTGACAGGCGAAGAGAGAGAA 360
 |||||
 DB 416 ATGACAGAAAGCTATCCAGGCTGTAGACAGACAGACTGACAGGCGAAGAGAGAA 475
 |||||
 QY 361 GAATTTAGTCCAACTTCAAAATTTATATATAGAGAGAAAGATGATGCTCTAC 420
 |||||
 DB 476 GAATTTAGTCCAACTTCAAAATTTATATATAGAGAGAAAGATGATGCTCTAC 535
 |||||
 QY 421 AACCCATCAATAAAGAAAGCAATGATTTTGACTATTTGAATCTAGGTAAAG 480
 |||||
 DB 536 AACCCATCAATAAAGAAAGCAATGATTTTGACTATTTGAATCTAGGTAAAG 595
 |||||
 QY 481 CACTTTTGGGAAAGTTATTTTGGTTGAGAGAAAGGCAATGGAAATATCATGCTATGA 540
 |||||
 DB 596 CACTTTTGGGAAAGTTATTTTGGTTGAGAGAAAGGCAATGGAAATATCATGCTATGA 655
 |||||
 QY 541 GATTCGAGAAAGAAAGTATTTTGCAGAAAGATGAAGTGCGCACACTCTAACTGAAG 600
 |||||
 DB 656 GATTCGAGAAAGAAAGTATTTTGCAGAAAGATGAAGTGCGCACACTCTAACTGAAG 715
 |||||
 QY 601 CAGAGATTAAGAAACACTAGACATCCCTTTTACATCTTGAATATTTCTCCAGAC 660
 |||||
 DB 716 CAGAGATTAAGAAACACTAGACATCCCTTTTACATCTTGAATATTTCTCCAGAC 775
 |||||
 QY 661 AAAAGACGTTTGTGTTTGTATGAGATATGTAATGGGCGAGACTGTTTCCATTT 720
 |||||
 DB 776 AAAAGACGTTTGTGTTTGTATGAGATATGTAATGGGCGAGACTGTTTCCATTT 835
 |||||
 QY 721 GTGAGAGAGCGGAGTCTTCTGAGAGCCGACACGTTTCTATGTGCGAAATGTCTC 780
 |||||
 DB 836 GTGAGAGAGCGGAGTCTTCTGAGAGCCGACACGTTTCTATGTGCGAAATGTCTC 895
 |||||
 QY 781 TGGCTTGAGCTATCTACATTCGAGAAAGTGTGTAACGTGATCTCAATGGAGATCT 840
 |||||
 DB 896 TGGCTTGAGCTATCTACATTCGAGAAAGTGTGTAACGTGATCTCAATGGAGATCT 955
 |||||
 QY 841 AATGCTGACAAAGATGGCCACATATAAATTAAGATTTTGGACTTTGCAAGAAAGGAT 900
 |||||
 DB 956 AATGCTGACAAAGATGGCCACATATAAATTAAGATTTTGGACTTTGCAAGAAAGGAT 1015
 |||||
 QY 901 CACAGATGACGCCACATGAAGACATTTCTGTGCACTCCAGAAATATCTGCAACAGAGT 960
 |||||
 DB 1016 CACAGATGACGCCACATGAAGACATTTCTGTGCACTCCAGAAATATCTGCAACAGAGT 1075
 |||||
 QY 961 GTTAGAAGATATGACTATGCGGAGCACTAGACTGTGTGGGCGCTTAGGGTTCTATGTA 1020
 |||||


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Db      1076 GTTAGAAGATTAAGTATGATGCGGACGATGAGCTGTGGGCTGTGGGTTGTATGTA 1135
Qy      1021 TGAATGATGTGGAGAGTTCCTTTCTACAAACCGACGACATGAGAACTTTTGAAAT 1080
Db      1136 TGAATGATGTGGAGAGTTCCTTTCTACAAACCGACGACATGAGAACTTTTGAAAT 1195
Qy      1081 AATATTATGAGAAACATTAATTTCTGGAACACTCTCTTGATGATGCAAAATCATTTGCT 1140
Db      1196 AATATTATGAGAAACATTAATTTCTGGAACACTCTCTTGATGATGCAAAATCATTTGCT 1255
Qy      1141 TTCAGGGCTCTTGATTAAGATTCGAAATTAAGCGCTTGTGTGAAGACGATGATGCANA 1200
Db      1256 TTCAGGGCTCTTGATTAAGATTCGAAATTAAGCGCTTGTGTGAAGACGATGATGCANA 1315
Qy      1201 AAAAAATTAGAGACACAGTTTCTCTCTGAGATTAACCTGCAAGATGTATGATTAATAA 1260
Db      1316 AAAAAATTAGAGACACAGTTTCTCTCTGAGATTAACCTGCAAGATGTATGATTAATAA 1375
Qy      1261 GCTTGACCTCTCTTTAAACCTCAAGTACATCTGAGACAGATTAATGATTTTGATGA 1320
Db      1376 GCTTGACCTCTCTTTAAACCTCAAGTACATCTGAGACAGATTAATGATTTTGATGA 1435
Qy      1321 AGAATTACAGCTCAGACTATTATTAACATTAACCCACCTGAAATATGATGAGATGTAT 1380
Db      1436 AGAATTACAGCTCAGACTATTATTAACATTAACCCACCTGAAATATGATGAGATGTAT 1495
Qy      1381 GGACTGCATGACCAATGAGA 1400
Db      1496 TGGCATGCTGTGGTAACTGGA 1515

```

RESULT 10

AAH79025

ID AAH79025 standard, cDNA, 1570 BP.

XX AAH79025;

DT 31-JAN-2002 (first entry)

XX Human Akt3 encoding cDNA SEQ ID NO 1.

XX Human; Akt3; AH/PH-domain containing serine/threonine kinase; Akt;
 KW cerebroprotective; neurotrophic; neuroprotective; antiarthritic;
 KW osteopathic; vasotrophic; hepatotrophic; inhibitor of apoptosis; ASK1;
 KW apoptosis stimulating kinase 1; hypoxia; necrosis; myocardial infarction;
 KW ischaemia reperfusion injury; stroke; organ transplantation;
 KW coronary artery bypass; tumour cell survival; gene therapy;
 KW Alzheimer's disease; osteoarthritis; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 126..1523

FT /tag= a

PN /product= "Akt3"

XX MO200168850-A2.

XX 20-SEP-2001.

XX 09-MAR-2001; 2001WO-US007663.

XX 14-MAR-2000; 2000US-00526043.

XX (AVERT) AVENTIS PHARM PROD INC.

XX Guo K, Pagnoni MF, Clark KL, Ivashchenko YD;

XX MPI: 2001-582452/65.

XX P-PSDB; AAG78018.

XX New nucleic acid encoding human Akt3 protein, useful for inhibiting cell

PT death and treating myocardial infarction, ischemia reperfusion injury
 PT associated with stroke, liver damage and renal failure.

PS Claim 1, Page 59-62; 73pp; English.

XX The invention relates to human Akt3 protein (AH/PH-domain containing
 CC serine/threonine kinase, Akt) comprising a fully defined sequence
 CC (AA478018) of 465 amino acids, its splice variant or allelic variant,
 CC where the encoding polynucleotide hybridizes under stringent conditions
 CC with a nucleic acid containing a nucleotide sequence (AAH79025) of 1570
 CC base pairs defined in the specification. Akt3 has cerebroprotective,
 CC neurotrophic, neuroprotective, antiarthritic, vasotrophic and
 CC hepatotrophic activity, as an inhibitor of apoptosis and/or apoptosis
 CC stimulating kinase 1 (ASK1)-induced cell death. Akt3 operably linked to a
 CC regulatory region is useful for inhibiting cell death in cardiac myocytes
 CC resulting from hypoxia, apoptosis or necrosis and for treating myocardial
 CC infarction or ischaemia reperfusion injury, particularly that associated
 CC with stroke, liver damage, renal failure, organ transplantation or
 CC coronary artery bypass grafting. Agonist of Akt3 are useful for improving
 CC Akt3 activity during treatment of patients suffering from myocardial
 CC infarction or ischaemia reperfusion injury and inhibitors of Akt3
 CC activity decrease tumour cell survival and result in tumour regression.
 CC Akt3 protects cells from apoptosis. Gene therapy using Akt3 reduces the
 CC quantity of cell death and final infarct size, resulting in improved post
 CC -infarction function, improved quality of life and reduced mortality. In
 CC patients with existing heart failure, gene therapy with Akt3 retards the
 CC process of ventricular dilation and slows down disease progression. Akt3
 CC gene therapy is useful for treating other disease states, involving cell
 CC death by apoptosis, including Alzheimer's disease, liver degeneration or
 CC osteoarthritis

SQ Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;

Query Match 88.2%; Score 1364.8; DB 4; Length 1570;

Best Local Similarity 98.4%; Pred. No. 0;

Matches 1378; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

```

Qy      1 GGGAGTCATCATGACGATGTTACCATTTGTGAAGAAAGTTGGTTCAAGAGGGGAGA 60
Db      116 GGGAGTCATCATGACGATGTTACCATTTGTGAAGAAAGTTGGTTCAAGAGGGGAGA 175
Qy      61 ATATATTAATAAACTGAGAGCCCAAGATCTCTTTTGAAGACAGATGCTCATTAAG 120
Db      176 ATATATTAATAAACTGAGAGCCCAAGATCTCTTTTGAAGACAGATGCTCATTAAG 235
Qy      121 AATATAAGAAAGAACTCAAGATGTGATTTACCTTATCCCTCAACACTTTTCAGTGGC 180
Db      236 AATATAAGAAAGAACTCAAGATGTGATTTACCTTATCCCTCAACACTTTTCAGTGGC 295
Qy      181 AAAATGCCAGTTAATGAAAAAGAAAGCAAGCAAGCAACATTTATATCATGATGCT 240
Db      296 AAAATGCCAGTTAATGAAAAAGAAAGCAAGCAAGCAACATTTATATCATGATGCT 355
Qy      241 CCAATGAGACTACTGTTATAGAGAAACATTTATGATGATTTCCAGAGAAAGGGAAGA 300
Db      356 CCAATGAGACTACTGTTATAGAGAAACATTTATGATGATTTCCAGAGAAAGGGAAGA 415
Qy      301 ATGACAGAAAGCTATCCAGGCTGTAGCAGACAGATGCAAGGCAAGAAAGAGAGAAAT 360
Db      416 ATGACAGAAAGCTATCCAGGCTGTAGCAGACAGATGCAAGGCAAGAAAGAGAGAAAT 475
Qy      361 GAATGTGATGCCAATTTCAAAATTTGATTAAGAGAGAAAGATGATGCTCTTAC 420
Db      476 GAATGTGATGCCAATTTCAAAATTTGATTAAGAGAGAAAGATGATGCTCTTAC 535
Qy      421 AACCATCATTAATAAGAAAGCAATGATGATTTGATTAATTTGAAACTAGTAAAG 480
Db      536 AACCATCATTAATAAGAAAGCAATGATGATTTGATTAATTTGAAACTAGTAAAG 595
Qy      481 CACTTTGGGAAAGTTATTTTGTGTCGAGAGAAAGCAAGTGAAGAAATCTATGCTATGA 540
Db      596 CACTTTGGGAAAGTTATTTTGTGTCGAGAGAAAGCAAGTGAAGAAATCTATGCTATGA 655

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QY	541	GATTCTGAAAGAAAGATCATTTATTCGAAGAGTAGTGGACACACTCTAATCTGAAAG	600
Db	656	GATTCCTGAAAGAAAGAGCATTTATTCGAAGAGTAGTGGACACACTCTAATCTGAAAG	715
QY	601	CAGAGTATTTAAAGAACACTAGACATCCCTTTTAACTATCCCTGAAATATTCCTCCAGAC	660
Db	716	CAGAGTATTTAAAGAACACTAGACATCCCTTTTAACTATTCCTGAAATATTCCTCCAGAC	775
QY	661	AAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGAGGAGCGAGCTGTTTTCCATTT	720
Db	776	AAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGAGGAGCGAGCTGTTTTCCATTT	835
QY	721	GTCGAGAGAGCGGGGTCTCTGAGAGCCGACACAGTTTCTATGAGTCAGAAATGTCTC	780
Db	836	GTCGAGAGAGCGGGGTCTCTGAGAGCCGACACAGTTTCTATGAGTCAGAAATGTCTC	895
QY	781	TGCCCTTGACCTATCTACATCCCGGAAAGATTTGTGATCCGTATCTCAAGTTGAGAAATC	840
Db	896	TGCCCTTGACCTATCTACATCCCGGAAAGATTTGTGATCCGTATCTCAAGTTGAGAAATC	955
QY	841	AATGCTGGAACAAGATGGCCACATPAAAAATTACAGATTTTGGACTTTGCAAGAGAGGAT	900
Db	956	AATGCTGGAACAAGATGGCCACATPAAAAATTACAGATTTTGGACTTTGCAAGAGAGGAT	1015
QY	901	CACAGATGCAAGCCACATGAAGACATTTGTGTGCACTCCAGAAATATCTGGACCAAGAGT	960
Db	1016	CACAGATGCAAGCCACATGAAGACATTTGTGTGCACTCCAGAAATATCTGGACCAAGAGT	1075
QY	961	GTTAAGAAATATATGACTATATGCGCGAGCAGTAGACTGTGGGGCCTTAGGGGTTGTCACTA	1020
Db	1076	GTTAAGAAATATATGACTATATGCGCGAGCAGTAGACTGTGGGGCCTTAGGGGTTGTCACTA	1135
QY	1021	TGAATATGATGTGTGGAGGTTACCTTTTCTACCAACGAGACCATGAGAACTTTTGAATT	1080
Db	1136	TGAATATGATGTGTGGAGGTTACCTTTTCTACCAACGAGACCATGAGAACTTTTGAATT	1195
QY	1081	AATATTTAATGGAAGACATTTAAATTTCTTCGAACTCTCTTCAGATGCAAAATCATTTGCT	1140
Db	1196	AATATTTAATGGAAGACATTTAAATTTCTTCGAACTCTCTTCAGATGCAAAATCATTTGCT	1255
QY	1141	TTTCAGGGCTCTTGATPAAAGAGATCCCAATPAAAGCCTTGTGTGAGAGACCAATGATGCATA	1200
Db	1256	TTTCAGGGCTCTTGATPAAAGAGATCCCAATPAAAGCCTTGTGTGAGAGACCAATGATGCATA	1315
QY	1201	AGAAATTTATGAGACACAGTTTCTCTCGAGTAATCTGGCAAGATGTATATGATPAAAAA	1260
Db	1316	AGAAATTTATGAGACACAGTTTCTCTCGAGTAATCTGGCAAGATGTATATGATPAAAAA	1375
QY	1261	GCTTGTACCTCCTTTTAAACCTCAAGTAACATCTGAGACAGATATCTAGATATTTTGTATGA	1320
Db	1376	GCTTGTACCTCCTTTTAAACCTCAAGTAACATCTGAGACAGATATCTAGATATTTTGTATGA	1435
QY	1321	AGAAATTTACAGCTCAGACTATTTACATPAAACACCACTGAAAAAATATGATGAGATGTAT	1380
Db	1436	AGAAATTTACAGCTCAGACTATTTACATPAAACACCACTGAAAAAATATGATGAGATGTAT	1495
QY	1381	GGAGCTGCATGCACATGAGA 1400	
Db	1496	TGGCAGTGTGTGGTAACTGGA 1515	
RESULT 11			
AAA89264			
ID	AAA89264 standard, cDNA, 1570 BP.		
AC	AAA89264;		
XX			
DT	28-MAR-2001 (first entry)		
XX			
DE	Human serine/threonine protein kinase Akt3 cDNA.		
Akt3; human; protein kinase; vascular endothelial growth factor; VEGF; inducer; ischemia; cardiomyopathy; angioemesis; tumour; gene therapy;			
KW			

Key	Location/Qualifiers
OS Homo sapiens.	
Key	126.1523
FT CDS	/*tag= a
WT	
PN WO200077190-A2.	
PD 21-DEC-2000.	
XX 01-JUN-2000; 2000WO-US015098.	
XX 11-JUN-1999; 99US-0138724P.	
PR 03-NOV-1999; 99GB-00026058.	
PA (AVET) AVENTIS PHARM PROD INC.	
PI Guo K, Ivashchenko Y, Clark K;	
DR WPI: 2001-025336/03.	
DR P-PSDB; AAB19996.	
PT Inducing expression of vascular endothelial growth factor, useful for	
PT treating an ischemic condition, e.g. cerebrovascular ischemia, renal	
PT ischemia or pulmonary ischemia, comprises administering a	
PT serine/threonine protein kinase Akt protein.	
PS Example 1; Page 55-58; 67pp; English.	
XX The present sequence is that of cDNA coding for human Akt3 (see	
XX AAB19996), a novel Akt isoform. Akt3 is a serine/threonine protein kinase	
CC capable of inducing vascular endothelial growth factor (VEGF) expression.	
CC The sequence was deduced from 2 cDNA clones isolated from a human heart	
CC cDNA library using a human Akt3 partial clone as probe. Akt3 is shorter	
CC than Akt1 (see AAB19997) and Akt2 (see AAB19998) and there is no	
CC significant homology between Akt3 and Akt1 or Akt2 at the C-terminus of	
CC the molecules. A claimed method of inducing expression of VEGF in a cell	
CC involves administering Akt1, Akt2 or Akt3, or a nucleic acid encoding	
CC such a protein. The cell is preferably from a patient suffering from an	
CC ischemic condition, especially cerebrovascular, renal, pulmonary, limb	
CC or myocardial ischemia, or ischemic, idiopathic or hypertrophic	
CC cardiomyopathy. The result is beneficial collateral blood vessel	
CC formation. A claimed method of inhibiting angiogenesis in a patient	
CC suffering from a tumour, comprises inhibiting the level of Akt activity	
CC in the patient, thereby inhibiting production of VEGF. The method	
CC comprises introducing an Akt antisense nucleic acid, an intracellular	
CC binding protein (e.g. a scfv) that specifically binds the Akt protein, or	
CC a nucleic acid encoding a dominant negative form of an Akt	
XX	
SQ Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;	
Query Match 88.2%; Score 1364.8; DB 4; Length 1570;	
Best Local Similarity 98.4%; Pred. No. 0;	
Matches 1378; Conservative 0; Mismatches 22; Indels 0; Gaps 0;	
QY 1 GGGAGTCATCATGAGCCATGTTACCATTTGTGAAAAGAGTTGGGTTCAAGAGAGGGAGA 60	
DB 116 GGGAGTCATCATGAGCCATGTTACCATTTGTGAAAAGAGTTGGGTTCAAGAGAGGGAGA 175	
QY 61 ATATATATAAAAGCTGAGAGCCAGATGATCTCTTTTGAAGACAGATGGCTCATTCATAGG 120	
DB 176 ATATATATAAAAGCTGAGAGCCAGATGATCTCTTTTGAAGACAGATGGCTCATTCATAGG 235	
QY 121 ATATATAAGAGAACTCAAGATGTGATTTTACCTTATCCCTCAACAATTTTCAGTGGC 180	
DB 236 ATATATAAGAGAACTCAAGATGTGATTTTACCTTATCCCTCAACAATTTTCAGTGGC 295	
QY 181 AAAATGCCAGTTAATGAAGACAGAACGACCAAGCCAAACATTTTATATCAAGATGCT 240	
DB 296 AAAATGCCAGTTAATGAAGACAGAACGACCAAGCCAAACATTTTATATCAAGATGCT 355	

Query Match 88.2%; Score 1364.8; DB 12; Length 1570;
 Best Local Similarity 98.4%; Pred. No. 0;
 Matches 1378; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 GGGAGTCATGATGAGCCATGTTACCATTTGTAAGAAAGTTGGTTGAGAAAGAGGGGAGA 60
 DB 116 GGGAGTCATGATGAGCCATGTTACCATTTGTAAGAAAGTTGGTTGAGAAAGAGGGGAGA 175

QY 61 ATATATATAAACTGGAGCCAAAGATCTCTCTTTGTAAGACAGATGGCTCATTAAGG 120
 DB 176 ATATATATAAACTGGAGCCAAAGATCTCTCTTTGTAAGACAGATGGCTCATTAAGG 235

QY 121 ATATATAAGAAACCTCAAGATGGATTTACCTTACCTTCAACAACTTTTCAGTGGC 180
 DB 236 ATATATAAGAAACCTCAAGATGGATTTACCTTACCTTCAACAACTTTTCAGTGGC 295

QY 181 AAAATGCCATTAATGAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 240
 DB 296 AAAATGCCATTAATGAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 355

QY 241 CCAATGAGTACTGTTTATGAGAGACATTTATGATGATCTCCAGAGAAAGAGAGAGA 300
 DB 356 CCAATGAGTACTGTTTATGAGAGACATTTATGATGATCTCCAGAGAAAGAGAGAGA 415

QY 301 ATGAGACAGAGCTATCCAGGCTGTAGAGACAGCTGAGAGAGAGAGAGAGAGAGAT 360
 DB 416 ATGAGACAGAGCTATCCAGGCTGTAGAGACAGCTGAGAGAGAGAGAGAGAGAGAT 475

QY 361 GAAATGTAGTCAACTTCACAAAATTTGATTAATATGAGAGAGAGAGAGATGCTCTAC 420
 DB 476 GAAATGTAGTCAACTTCACAAAATTTGATTAATATGAGAGAGAGAGATGCTCTAC 535

QY 421 AACCCATCATTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 480
 DB 536 AACCCATCATTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 595

QY 481 CACTTTGGGAAAGTTATTTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 540
 DB 596 CACTTTGGGAAAGTTATTTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 655

QY 541 GATTTGTAAGAAAGAAAGTCAATTAATGCAAGAGATGAGAGAGAGAGAGAGAGAG 600
 DB 656 GATTTGTAAGAAAGAAAGTCAATTAATGCAAGAGATGAGAGAGAGAGAGAGAGAG 715

QY 601 CAGAGTATTAAGAAACCTAGACATCCCTTTTAACTCTTGAATATTTCTTCCAGAC 660
 DB 716 CAGAGTATTAAGAAACCTAGACATCCCTTTTAACTCTTGAATATTTCTTCCAGAC 775

QY 661 AAAAGACCGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 720
 DB 776 AAAAGACCGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 835

QY 721 GTGAGAGAGAGGGGTTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 DB 836 GTGAGAGAGAGGGGTTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 895

QY 781 TGCCTTGAGTATCTACATTCGCGAAAGATTTGTATCCGTGATCTCAAGTTGAGAAAT 840
 DB 896 TGCCTTGAGTATCTACATTCGCGAAAGATTTGTATCCGTGATCTCAAGTTGAGAAAT 955

QY 841 AATGCTGGAAGAAAGATGAGCAATTAATTAAGATTTGAGAGAGAGAGAGAGAGAG 900
 DB 956 AATGCTGGAAGAAAGATGAGCAATTAATTAAGATTTGAGAGAGAGAGAGAGAGAG 1015

QY 901 CACAGATGAG 960
 DB 1016 CACAGATGAG 1075

QY 961 GTTGAAGATATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 DB 1076 GTTGAAGATATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1135

QY 1021 TGAATATATGATGAT 1080

DB 1136 TGAATATATGATGAT 1195
 QY 1081 AATATTAATGAGAAAGACATTAATTTCTCGAAACATCTCTTCAGATGACAAATCATTTGCT 1140
 DB 1196 AATATTAATGAGAAAGACATTAATTTCTCGAAACATCTCTTCAGATGACAAATCATTTGCT 1255

QY 1141 TTCAAGGCTCTTGATTAAGATTCGAATTAAGCCCTTGGTGGAGAGACAGATGATGCAAA 1200
 DB 1256 TTCAAGGCTCTTGATTAAGATTCGAATTAAGCCCTTGGTGGAGAGACAGATGATGCAAA 1315

QY 1201 AGAAATTAAGAGACAGATTTCTTCTGAGAGTAACTGGCAAGATGATATATGATTAATA 1260
 DB 1316 AGAAATTAAGAGACAGATTTCTTCTGAGAGTAACTGGCAAGATGATATATGATTAATA 1375

QY 1261 GCTTGATCTCTCTTTTAACTTCAGATTAATCTGAGAGACATCTAGATATATTTGATGA 1320
 DB 1376 GCTTGATCTCTCTTTTAACTTCAGATTAATCTGAGAGACATCTAGATATATTTGATGA 1435

QY 1321 AGAATTTACAGCTCAAGATTTTCAATTAACCACTGAAATAATGATGAGAGATGAT 1380
 DB 1436 AGAATTTACAGCTCAAGATTTTCAATTAACCACTGAAATAATGATGAGAGATGAT 1495

QY 1381 GGACTGATGAGACATGAGA 1400
 DB 1496 TGGCATGCTGGTACTGGA 1515

RESULT 13
 ADN71941
 ID ADN71941 standard; cDNA; 2277 BP.
 XX
 AC ADN71941;
 DT 12-AUG-2004 (first entry)
 XX
 DE Chicken serine/threonine protein kinase (akt1) encoding cDNA SEQ ID:27.
 XX
 KW kinase pathway inhibitor; anti-prostate cancer;
 KW mitogen-activated protein kinase pathway inhibitor;
 KW MAP kinase pathway inhibitor; prostate cancer inhibitor;
 KW phosphatidylinositol 3-kinase/Akt kinase pathway;
 KW PI3K/Akt kinase pathway; cytoskeletal; MAP kinase inhibitor;
 KW phosphatidylinositol 3-kinase/Akt kinase inhibitor;
 KW PI3K/Akt kinase inhibitor; androgen receptor inhibitor; prostate cancer;
 KW chicken; serine/threonine protein kinase; akt1; gene; ss.
 XX
 OS Gallus gallus.
 XX
 FH Key Location/Qualifiers
 FT 466..1908
 FT /*tag= a
 FT /product= "serine/threonine protein kinase (akt1)"
 XX
 PN MO2004041185-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 31-OCT-2003; 2003WO-US034636.
 XX
 PR 31-OCT-2002; 2002US-0423340P.
 XX
 PA (UYRP) UNIV ROCHESTER.
 XX
 PI Chang C, Lee Y, Lin W;
 XX
 DR WPI: 2004-390508/36.
 DR P-PSDB; ADN71942.
 XX
 PT Composition useful in the treatment of e.g. prostate cancer comprises a
 XX kinase pathway inhibitor and an anti-prostate cancer compound.
 PS Disclosure; SEQ ID NO 27; 118bp; English.

FT /product= "protein_kinase_B"
 XX
 PN WO200020025-A2.
 XX
 PD 13-APR-2000.
 XX
 PF 29-SEP-1999; 99WO-US022633.
 XX
 PR 02-OCT-1998; 98US-0102740P.
 XX
 PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
 XX
 PI Walsh K;
 XX
 DR WPI, 2000-303639/26.
 DR P-PDB; AAY92223.
 XX
 PT Treating myocardial infarction or conditions associated with increased
 PT apoptotic cell-death of vascular endothelial cells or skeletal myocytes
 PT comprises administering Akt (also termed Protein Kinase B (PKB))
 PT molecule.
 XX
 PS Disclosure; Page 69; 71pp; English.
 XX
 CC The invention concerns methods of treating myocardial infarction, which
 CC comprise administering to a subject an Akt (Protein Kinase B) molecule to
 CC inhibit cardiac tissue necrosis. Akt is a proto-oncogene which encodes a
 CC serine threonine kinase. It inhibits apoptotic cell death, in particular
 CC of cardiomyocytes, skeletal myocytes and/or vascular endothelial cells.
 CC It is therefore also useful for treating muscular dystrophy, spinal
 CC muscular atrophy, anabolic steroid-induced muscle injury, skeletal muscle
 CC oxidative stress, physical exercise and unloading-induced skeletal muscle
 CC atrophy. The Akt protein can also be used in screening for an inhibitory
 CC agent that inhibits apoptotic cell-death of cells
 CC
 SQ Sequence 2626 BP; 584 A; 767 C; 754 G; 521 T; 0 U; 0 Other;
 Query Match 48.6%; Score 751.4; DB 3; Length 2626;
 Best Local Similarity 71.8%; Pred. No. 3.2e-193;
 Matches 1044; Conservative 0; Mismatches 396; Indels 15; Gaps 4;
 QY 8 ATCATGAGCGATGTTACATTGTGAAGAAGGTTGGCTCAGAAAGAGGAGATATATA 67
 DB 281 ACCATGAACAGCTAGCATTTGTGAAGAGGCGCTGCGACAAACAGAGGGAATATATT 340
 QY 68 AAAAAGTGAAGGCGAAGATATCTTCTTTGAAGACAGATGGCTCATTCATAGATATATA 127
 DB 341 AAAACGTGGCGGCGACGCTACTTCTCTCAAGAACATGGCACTTTATTGGCTACAG 400
 QY 128 GAGAAACCTCAAGATGGAT--TTACCTTATCCCTCAACAACTTTCAATGAGCAAA 184
 DB 401 GAACGGCTCAGATGGATGATCAGCGAGATCCCACTCAACAACTTCTCAATGAGCAAA 460
 QY 185 TGCAGTTTAATGAAGACAGAACGACAAAGCCAAACATTTATATCATGATGTCAG 244
 DB 461 TGCAGCTGATGAAGACAGAGCGGCCAAAGCCCAACCTTTATCATCCGCTGCTGAG 520
 QY 245 TGGACCACTGTTATAGAGAACTTTATGATGATCTCAGAGGAAAGGAAAGATGG 304
 DB 521 TGGACCACTGATTTAGGCGCACTTCCATGTGAAACGCTGAGGAGCGGAAAGATGG 580
 QY 305 ACGAAGCTATTCAGGCTGTGACAGACACTGCAAGGCGCAAGAGAGAGAGATGAT 364
 DB 581 GCCACGGCCATTCAGATCTGTGGCGGATGACTCAAGAGGCGAGAGAGAGAGAGATGAC 640
 QY 365 TGTAGTCAACTTCACAATTTGATATATATAGAGAGAGAGATGATGATGCTTCAACAC 424
 DB 641 TTCCGATCAGGCTCACCAGTACACTCAGGGGCTGAAGAGATGAGGATGCTCCCTGACC 700
 QY 425 CATC--ATAAAAGAAAGACATGATGATTTGACTATTGTAATCTAGTAAAGGC 481
 DB 701 AAGCCCAAGACCGGTGACCATGAAAGAGTTTGAAGTGAAGTAACTAGGCAAGGC 760

QY 482 ACTTTGGGAAGTATTTTGTGAGAGAGGCAAGTGGAATACTATGCTATGAAG 541
 DB 761 ACCTTGGGAAATGATTTCTGTGAAGAGAAAGCCACAGCGCTCATATGCAATGAAG 820
 QY 542 ATTCTGAAGAAAGAGTCAATTTATGCAAGAGATGAGGACACACTCACTGAAGC 601
 DB 821 ATCTTCAAGAGAGAGGTCATCGCGCCAGAGATGAGGTTGCCACACGCTTATGAGAAC 880
 QY 602 AGAGTATTAAGAACATAGACATCCCTTTTAAACATCCTTGAATATTCCTTCAGACA 661
 DB 881 CGTGTCTGCAAGACTCTAGGCACTCCCTTCTTACCGGCCCTCAAGTACTCATTCAGACC 940
 QY 662 AAGACCGTTTGTGTTTGAATGAGAAATATTAAGGGGGGAGAGCTTTTCCATTG 721
 DB 941 CACGACCGCTCTGCTTTGTGATGAGATGCGCAACGAGGGGAGAGCTTCTTCACTG 1000
 QY 722 TCAGAGAGGCGGTGTTCTCTGAGACCCGACACAGTTTCTATGAGTCAAGAAATGCTCT 781
 DB 1001 TCTCGAAGAGCGCGTGTCTTCCAGAGACCGGGCCGCTTCTATGTTGCGAGATTTGTCT 1060
 QY 782 GCGTGTGACTATCTAATTCGGAAGA--TTGTGTACCGTATCTCAAATTGAGAAAT 838
 DB 1061 GCCCTGGAATCTTGCACTCCGAGAAAGAGTGTGTACCGGAGACTGGAAGCTGGAAC 1120
 QY 839 CTAACTGTGACAAAGATGCGCACATTAATAATTCAGATTTTGGACTTTGCAAGAAAGG 898
 DB 1121 CTATCTGTGACAAAGACGCGCACATCAAGATACGACTTCGCGCTGTGCAAGAGGG 1180
 QY 899 ATCAGAGATGAGCCGACATTAAGAGATCTTGTGAGACTTCAGAAATATCTGACACAG 958
 DB 1181 ATCAAGATGATGCTCATTAAGAGATCTTGTGGAACCGCGAGATACCTGGCCCTGAG 1240
 QY 959 GTGTTAAGATATATGACTATGAGCGGAGAGTACTGTGTGGGCTTGAAGGTTGTGATG 1018
 DB 1241 GTGCTGAGAGCAACACACTACGCGCGTGCAGTGTGATGAGTGTGGGCGTGGCTCATG 1300
 QY 1019 TATGAATGATGTGTGAGAGTGTACCTTCTTAAACAGAGACGATGAGAACTTTTGA 1078
 DB 1301 TATGAATGATGTGTGAGAGTGTACCTTCTTAAACAGAGACGATGAGAACTTTTGA 1360
 QY 1079 TTAATATTAATGAGAACTTAATTTCTGCAACACTCTCTTCAATGCAAAATGATTTG 1138
 DB 1361 CTGATCTCATGAGAGAGATCCGCTTCCGCGACACTCGGCCCTGAGGCAAGTCCCTG 1420
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 QY 1319 GAAGAATTAACAGTCAAGCTATTAATTAATTAACCACTGAAAAATATGATGAGATG 1378
 DB 1601 GAGAGATTAACAGCTCAAGTATCAATCAACGCGCCCTG-----ATCAAGATGACAGC 1654
 QY 1379 ATGAGCTGATGAGACATGAGAGCGCGGCAATTTCCCTCAATTTCTTCTGAGAT 1438
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 QY 1439 GAGAGAAATTAAGTC 1453
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 RESULT 15
 AAD28550
 ID AAD28550 standard; cDNA; 2626 BP.
 XX

AC AAD28550;
XX
DT 07-MAY-2002 (first entry)
XX
DE Mouse Akt cDNA.
XX
KW Mouse; 3-hydroxy-3-methylglutaryl-coenzyme A reductase inhibitor;
KM HMG-CoA; angiogenesis; Akt protein; serine-threonine kinase; PKB;
KM protein kinase B; vascular insufficiency; nonhypercholesterolaemic;
KM nonhyperlipidaemic; hypertension; vascular disease; gangrene; wound;
KM Buerger's syndrome; myocardial infarction; coronary artery disease;
KM ischaemia; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 284..1726
FT /tag= a
FT /product= "Mouse Akt protein"
XX
PN MO200193806-A2.
XX
PD 13-DEC-2001.
XX
PF 05-JUN-2001; 2001WO-US018175.
XX
PR 08-JUN-2000; 2000US-00590740.
XX
PI (SELI-) ST ELIZABETH'S MEDICAL CENT BOSTON INC.
XX
PI Walsh K;
XX
DR WPI: 2002-164293/21.
XX
PT P-PSDB; AAE17784.
XX
PT Use of 3-hydroxy-3-methylglutaryl-coenzyme A reductase inhibitor in
PT promoting angiogenesis in a tissue of a subject to treat conditions e.g.
XX hypertension.
XX
PS Disclosure; Page 68-69; 70pp; English.
XX
CC The invention relates to 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA)
CC reductase inhibitors and their use in promoting angiogenesis and in
CC activating Akt polypeptides in vascular endothelial cells. Akt is a proto
CC oncogene encoding a serine-threonine kinase (also known as protein
CC kinase B, PKB). The invention also relates to methods and compositions
CC for the treatment of conditions associated with vascular insufficiency.
CC HMG-CoA reductase inhibitors are used for treating nonhyperlipidaemic and
CC /or nonhypercholesterolaemic subjects who are in need of increased blood
CC flow to a tissue or promoting angiogenesis, to treat conditions such as
CC hypertension, diabetic peripheral vascular disease, gangrene, Buerger's
CC syndrome, wound (e.g. surgical wound), ischaemia of the muscle, brain,
CC kidney, lung, heart and limb, severe occlusive and/or obstructive
CC vascular disease, peripheral vascular disease, myocardial ischaemia,
CC myocardial infarction, coronary artery disease, cerebral vascular disease
CC and visceral vascular disease. The present sequence is mouse Akt cDNA
XX
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Query Match 48.6%; Score 751.4; DB 6; Length 2626;
Best Local Similarity 71.8%; Pred. No. 3.2e-193;
Matches 1044; Conservative 0; Mismatches 396; Indels 15; Gaps 4;
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QY 128 GAGAAACCTCAAGATGGAT--TTACCTTATCCCTCAACAACCTTTCAAGTGGCAAA 184

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DB 461 TGGCAGCTGATGAAGACAGAGCGGCTCAAGGCCCAACCTTTATATATCGCTGCGAG 520
QY 245 TGGACTACTGTATATAGAGAAACATTTCAATGATTAATCTCCAGAGAAAGGAAATATG 304
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OM nucleic - nucleic search, using sw model

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SUMMARIES

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2	751.4	48.6	2626	4 US-09-590-740-5	Sequence 138, App
3	721.2	46.6	2184	4 US-09-417-197-138	Sequence 1, Appl1
4	719.2	46.5	2610	2 US-09-212-771-1	Sequence 1, Appl1
5	719.2	46.5	2610	3 US-09-091-058-1	Sequence 1206, Ap
6	719.2	46.5	2610	4 US-09-023-655-1206	Sequence 1, Appl1
7	719.2	46.5	2610	4 US-09-590-740-1	Sequence 70, Appl
8	716.4	46.3	2181	4 US-09-417-197-70	Sequence 1, Appl1
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15	266.4	12.8	2239	4 US-09-949-016-1676	Sequence 1471, Ap
16	261.2	16.9	3255	4 US-09-016-434-1471	Sequence 2007, Ap
17	261.2	16.9	6102	4 US-09-949-016-2007	Sequence 1, Appl1
18	260.4	16.8	2370	3 US-09-031-895-1	Sequence 2948, Ap
19	260.2	16.8	265	4 US-09-513-999C-2948	Sequence 1, Appl1
20	258.8	16.7	1338	4 US-10-067-977-1	Patent No. 526464
21	257.6	16.7	2599	6 526464-1	Patent No. 526464
22	257.6	16.7	2599	6 526464-1	Patent No. 526464
23	257.2	16.6	2311	3 US-08-712-709-6	Sequence 6, Appl1
24	257.2	16.6	2311	3 US-09-111-444-6	Sequence 6, Appl1
25	257.2	16.6	2311	3 US-09-541-228-6	Sequence 772, App
26	257.2	16.6	2311	4 US-09-016-434-772	Sequence 1735, Ap
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28	250.4	16.2	2245	3 US-09-225-749-24	Sequence 24, Appl
29	246.4	15.9	3321	4 US-09-023-655-1361	Sequence 1361, Ap
30	241.4	15.6	2244	4 US-09-094-714A-48	Sequence 48, Appl
31	240.8	15.6	2274	4 US-09-772-647-3	Sequence 3, Appl1
32	238.6	15.4	532	4 US-09-270-767-14090	Sequence 14090, A
33	233.2	15.1	2556	4 US-09-817-310-1	Sequence 1, Appl1
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35	229.8	14.9	1413	4 US-09-248-796A-4379	Sequence 4379, Ap
36	225.4	14.6	2127	4 US-09-270-767-13509	Sequence 13509, A
37	222.6	14.4	2751	4 US-09-417-197-72	Sequence 72, Appl
38	222.4	14.4	2346	4 US-09-762-258-3	Sequence 3, Appl1
39	218	14.1	2324	4 US-09-190-976B-6	Sequence 6, Appl1
40	214.6	13.9	2705	4 US-09-949-016-839	Sequence 839, App
41	214.6	13.9	2715	4 US-09-949-016-1959	Sequence 1959, Ap
42	213	13.8	2754	4 US-09-429-322-3	Sequence 3, Appl1
43	211.6	13.7	2946	4 US-09-949-016-1991	Sequence 1991, Ap
44	211.6	13.7	4438	4 US-09-566-921-81	Sequence 81, Appl
45	206.6	13.4	2262	4 US-09-949-016-5805	Sequence 5805, Ap

ALIGNMENTS

RESULT 1									
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Patent No. 6809194									
GENERAL INFORMATION:									
APPLICANT: Reinhard, Christoph									
APPLICANT: Jefferson, Anne B.									
TITLE OF INVENTION: AK3 INHIBITORS									
FILE REFERENCE: PP-01699.002/200130.520									
CURRENT APPLICATION NUMBER: US/09/851,670									
NUMBER OF SEQ ID NOS: 27									
SOFTWARE: FastSeq for Windows Version 4.0									
SEQ ID NO 1									
LENGTH: 1547									
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QY	361	GAATGTAGTCCAACTTCAAAATGATATATAGAGAGAGAGATGATGCTCTAC	420						
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 US-09-590-740-5
 ; Sequence 5, Application us/09590740
 ; Patent No. 6689807
 ; GENERAL INFORMATION:
 ; APPLICANT: Kenneth Walsh
 ; APPLICANT: St. Elizabeth's Medical Center
 ; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
 ; FILE REFERENCE: 49,784 (1417)
 ; CURRENT APPLICATION NUMBER: US/09/590,740
 ; CURRENT FILING DATE: 2000-06-08
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 2626
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QY 1074 TTGAATTAATTAATGAGAAACATTAAATTTCTGAAACCTCTCTTCAATGCAAAAT 1133
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QY 1134 CATTGCTTCAAGGCTCTTGATTAAGATCCAAATTAAGCCCTTGCTGAGAGACCAAGT 1193
DB 1874 CCTTGCTTCAAGGCTGCTGCTGAGAGAGACCCCAAGAGAGCTTGCGGGGCTCCGAGG 1933
QY 1194 ATGCAAAAGAAATTAATGAGACACAGTTCTCTCTGAGTAACTGCAAGATGATATG 1253
DB 1934 AGCCCAAGAGATGATGAGCAGCATCGCTTCTTGCGGTATCGTGTGCGAGCAGTGTAG 1993
QY 1254 ATAAAGCTTGACTCTCTTTTAACTCAAGTAACTGAGACAGATPACTGATATT 1313
DB 1994 AGAAGAGCTCAGCCCACTTCAGCCCGAGGTCAAGTCAAGTCAAGCAGCATGATATT 2053
QY 1314 TTGATGAGATTTAGAGCTGACGATTAATTAACAAATACCACTGAAATTAATGAGAG 1373
DB 2054 TTGATGAGATTTAGAGCTGACGCGCCCAAGATTAATCACTGAGCACTGAGCA--GAGT 2107
QY 1374 ATGATGAGCTGATGAGCAATGAGAGCGCGCATTTCTCAATTTCTTACTCTG 1433
DB 2108 ACAGCATGAGGTGTGTGAGACGAGGAGCGAGGCCCACTTCCCGAGTTCTCTACTCG 2167
QY 1434 CAGG 1437
DB 2168 CCAG 2171

RESULT 4
US-09-212-771-1
Sequence 1, Application US/09212771
Patent No. 5958773
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
FILE REFERENCE: RFS-0034
CURRENT APPLICATION NUMBER: US/09/212,771
CURRENT FILING DATE: 1998-12-16
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
LENGTH: 2610
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (199)..(1641)
US-09-212-771-1

Query Match 46.5%; Score 719.2; DB 2; Length 2610;
Best Local Similarity 70.3%; Pred. No. 4.3e-206;
Matches 1025; Conservative 0; Mismatches 418; Indels 15; Gaps 4;

QY 5 GTCATATGAGCGATGTACCATTTGGAAGAAAGTTGGCTTCAAGAGGGAGAAATAT 64
DB 193 GGCACCATAGAGCACTGGCTATTGTGAAGAGGTTGGCTGACAAAGAGGGAGTAC 252
QY 65 ATAAAGCTGAGGCGCAAGATACCTTTTGAAGACAGATGGCTATTCAATGAGATAT 124
DB 253 ATCAAGCTTGGCGGCGCAAGCTTCTCTCTCAAGAAATGATGCGACCTTCATGGCTAC 312

QY 125 AAGAGAAACCTCAAGATGTGATTTACTTTA---TCCCTTCAGCACTTTCACTGAGCA 181
DB 313 AAGAGCGGCGCGCAGATATGAGCAAGTGAAGCTCCCTTCAGCACTTTCTGTGGG 372
QY 182 AATATGCACTTAATGAAACAGACAGCAAGCCAAACACTTTATATCATGATGTCTC 241
DB 372 CAGTCCAGCTGATAGAGAGCGAGCGGCCCGGCCCAACACTTATCATCTGCTGCTG 432
QY 242 CAGTGAATCTGTTATAGAGAACTTTCACTGATATCTCCAGAGGAAAGAGAA 301
DB 433 CAGTGAATCTGTTATAGAGAACTTTCACTGATATCTCCAGAGGAAAGAGAA 492
QY 302 TGAAGAGAGCTATTCAGGCTGTAGCAGACACTGCAAGGCAAGAGAGAGAGATG 361
DB 492 TGAAGAGAGCTATTCAGGCTGTAGCAGACACTGCAAGGCAAGAGAGAGAGATG 552
QY 362 AATGTATGCTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 421
DB 552 GACTTCCGCTCGGGCTCAGCCAGTGAACCTCAGGGGCTGAAGAGATGAGGTGTCCTG 612
QY 422 ACCCATC--ATAAAGAAAGCAATGATGATTTTGAATTTGAACTAATGAACTA 478
DB 613 GCCAAGCCAGACACCGCTGTGACATGACAGATTTGAGTACTGAGCTGCTGGGCAAG 672
QY 479 GGCACCTTTGGGAAATTTTGTGCGAGAGAGGCAAGTGAATAATCTATGCTATG 538
DB 672 GGCACCTTTGGGAAATTTTGTGCGAGAGAGGCAAGTGAATAATCTATGCTATG 732
QY 539 AAGATTTGAGAAAGAAAGTCAATTTGCAAGAGATGAGTGCACACTTAACTGAA 598
DB 733 AAGATTTGAGAAAGAAAGTCAATTTGCAAGAGATGAGTGCACACTTAACTGAA 792
QY 599 AGCAGATTTTAAAGCACTAGACATCCCTTTTAACTCTGAAATATCTCTGAG 658
DB 793 AACCGCTCTCAGAACTCAGGAGACCCCTTCTCAGAGCTTCAAGCTCTTCTCAG 852
QY 659 ACAAAGACCGTTGT 718
DB 853 ACCCAAGACCGCTCTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 912
QY 719 TTGTGAGAGAGCGGCTGTCTGTGAGACCGGCAACGTTTCTATGTGCGAAGATGTG 778
DB 913 CTGTCCCGGAAACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 972
QY 779 TCTGCTTGAATATATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 835
DB 973 TACGCTTGAATATATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT 1032
QY 836 AATCTAATGCTGAGCAAGAGATGCGCAATTAATTAATTAATTAATTAATTAATTA 895
DB 1033 AACTCATGCTGAGCAAGAGATGCGCAATTAATTAATTAATTAATTAATTAATTA 1092
QY 896 GGGATCAAGATGAGCGCCATGAAAGCAATTTCTGTGCACTTCCAGAAATATTTGCA 955
DB 1093 GGGATCAAGATGAGCGCCATGAAAGCAATTTCTGTGCACTTCCAGAAATATTTG 1152
QY 956 GAGGTGTTAAGATATATGACTATGCGGAGAGAGAGTGTGAGGCTGAGGCTGCTGTC 1015
DB 1153 GAGGTGTTAAGATATATGACTATGCGGAGAGAGAGTGTGAGGCTGAGGCTGCTGTC 1212
QY 1076 GAATTAATTAATGAGAGCAATTAATTTCTGCAACACTCTCTTCAATGCAAAATCA 1135
DB 1273 GAGCTATCTCATGAGAGAGATCCGCTTCCGCGCAAGCTTGTGTCGAGGCAAGTCC 1332
QY 1136 TTGCTTTGAGGCTCTTGTAAAGATCAAAATTAAGCGCTGTGAGAGACCAAGATAT 1195
DB 1333 TTGCTTTGAGGCTCTTGTAAAGATCAAAATTAAGCGCTGTGAGAGACCAAGATAT 1392
QY 1196 GCAAAAGAAATTAATGAGACAGATTTCTTCTGAGATTAAGTGGCAAGATGATATGAT 1255

QY 1436 AGTGACGAGAAATAGTC 1453
DB 1627 AGCAGACGCGCTGAGGC 1644

RESULT 6

US-09-023-655-1206
Sequence 1206, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1206:
SEQUENCE CHARACTERISTICS:
LENGTH: 2610 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9190827
US-09-023-655-1206

Query Match 46.5%; Score 719.2; DB 4; Length 2610;
Best Local Similarity 70.3%; Pred. No. 4.3e-206;
Matches 1025; Conservative 0; Mismatches 418; Indels 15; Gaps 4;

QY 5 GTCATATAGAGCATTTTACCATTTGGAAGAAGTTGGCTTCAGAAAGGGGAGCATAT 64
DB 193 GGCACCATAGACGACCTGGCTATTGGAAGAGGTTGGCTGCACAAAGAGGGAGTAC 252
QY 65 ATAAAAAATGAGAGCGCAAGATACCTCTTTGGAAGACAGATGGCTCATTCATAGATAT 124
DB 253 ATCAAGACCTGGCGGCGACGCTACTTCTCTCAAGAAATGATGCACTTTCATTGCTAC 312
QY 125 AAAGAGAAACCTCAAGATGTGATTTTACCTTA---TCCCTCAACAACCTTTTCAGTGCA 181
DB 313 AAGAGACGCGCGCAGAGATGTGACCAACGAGAGGCTCCCTCAACAACCTTCTGTGGCG 372
QY 182 AATGCGCATTTATGAAAACAGAAAGCAAGAGCCAAACATTTTATTCAGATGTCTC 241
DB 373 CAGTGCAGACTGATGAAGACGAGCGGCCCGGCCCAACACCTTCATTCGCTGCGCTG 432

QY 242 CAGTGAACACTACTGTATAGAGAGACATTTTCATGTAGATTAATCCAGAGAAAGGAAGA 301
DB 433 CAGTGAACACTACTGTATAGAGAGACATTTTCATGTAGATTAATCCAGAGAGGAGAGAG 492
QY 302 TGGACGAAGACTATTCAGGCTGTAGCAGACAGACTGACAGAGCAAGAAAGAGAGAAATG 361
DB 493 TGGACGAAGACTATTCAGGCTGTAGCAGAGAGAGAGAGAGAGAGAGAGAGAGATG 552
QY 362 AATGTAGTCCAACTTCAAAATTTGATTAATATAGAGAGAGAGAGAGATGAGTCCCTACA 421
DB 553 GACTTCGGGTGGGCTCAACCCAGTGAACATCTAGGGGCTGAAGAGATGAGTGTCCCTG 612
QY 422 ACCCAT---ATAAAAGAAAGACATGATGATTTTGACTATTGAACTAGATGATAA 478
DB 613 GCCAAGCCCAAGCACCAGGTGACATGAAAGAGTTTGAAGTACTGATGAGTGTGGGCAAG 672
QY 479 GGCACCTTTGGAAAATTAATTTGGTTGAGAGAAAGCAAGTGAATAATCTATGCTATG 538
DB 673 GGCACCTTTGGCAAGTATCTGGTGAAGAGAGCAAGCGCGCTACTACGCCATG 732
QY 539 AAGATTCGAAGAAAGAGTCTATTATGCAAGAGTGAAGTGGACACACTTAATCTGAA 598
DB 733 AAGATTCGAAGAAAGAGTCTATTATGCAAGAGTGAAGTGGACACACTTAATCTGAA 792
QY 539 AAGATTCGAAGAAAGAGTCTATTATGCAAGAGTGAAGTGGACACACTTAATCTGAA 658
DB 793 AACCGGTCTGCAAGAACTCCAGAGCACTCCCTTCCACAGCCCTGAAGTACTTTCCAG 852
QY 659 ACAAAGACCGTTGTGTGTTGTGTGATGGAATATGTTAAATGGGGGCGAGCTGTTTCAT 718
DB 853 ACCCAAGACCGCTGCTTGTGTGATGGAATATGTTAAATGGGGGCGAGCTGTTTCAC 912
QY 719 TGTGAGAGAGCGGGGTGTCTGTGAGACCGGCAACGTTTCTATGTGAGAAATGTGC 778
DB 913 CTGTCCGGGAAAGTGTGTGTCTGAGAGACGGGCGCCCTCTTATGTGAGGCTGAGATGTG 972
QY 779 TCTGCTTGAACATATCTACATCCGGAAGA---TTGTGTACCGGTATCTCAAGTTGAG 835
DB 973 TCAAGCTGTGACTACTGTGACCTCGGAGAAAGACGTGTGTACCGGGAGCTCAAGCTGAG 1032
QY 836 AATCTAATGTGAGCAAGATGCGCAATTAATAATTAAGATTTTGAAGCTTTCAGAAAGA 895
DB 1033 AACTCATGTGTGAGCAAGAGCGGCAATTAAGATCAAGACTTGGGCTGTGCAAGGAG 1092
QY 896 GGGATCAGAGTGCAGCAACCAATGAAGCATTTGTGTGCACTCCGAATATCTGACACA 955
DB 1093 GGGATCAGAGTGCAGCAACCAATGAAGCATTTGTGTGCACTCCGAATATCTGACACA 1152
QY 956 GAGGTGTGAAGATATGACTATGCGGAGAGCTGAGTGAAGTGGGCTGAGGAGTGTGC 1015
DB 1153 GAGGTGTGAGAGCAATGATGATGCGGCGGTGAGTGAAGTGGGCTGAGGAGTGTGC 1212
QY 1016 ATGTATGAAGATGTGTGGAGGTTTACCTTTTCAACAACAGACCATATGAGAACTTTT 1075
DB 1213 ATGTATGAAGATGTGTGGAGGTTTACCTTTTCAACAACAGACCATATGAGAACTTTT 1272
QY 1076 GAATTAATTAATGAGAGCAATTAATTTCTGCAACACTCTCTTCAGATGCAAAATCA 1135
DB 1273 GAGGTATCTCATGAGAGAGATTCGCTTCCGCGCAAGCTTGTGTCGAGGCGCAAGTCC 1332
QY 1136 TTGCTTTCAAGGCTCTTGTATTAAGATCAAAATAACCTTTGTGAGAGACCAATGAT 1195
DB 1333 TTGCTTTCAAGGCTCTTGTATTAAGATCAAAATAACCTTTGTGAGAGACCAATGAT 1392
QY 1196 GCAAAAGAAATTAATGAGACACATTTCTTCTGTGAGTAACTGGCAAGATATATGAT 1255
DB 1393 GCAAGAGATCATGAGATGATGCTTTTGTGCGGTATCGTGTGACACAGTGTACAG 1452
QY 1256 AAAAGCTTGTATCTCTTTTAACTCAAGTAAATCTGAGACAGATATCTAATATTT 1315
DB 1453 AAGAGCTCAAGCCACCTTCAAGCCCAAGGTCAAGTGTGAGAGATGACACCAAGATATTT 1512


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; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 70
; LENGTH: 2181
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PKB-EGFP fusion
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2178)
US-09-417-197-70

Query Match      46.3%; Score 716.4; DB 4; Length 2181;
Best Local Similarity 70.7%; Pred. No. 2,7e-205;
Matches 1015; Conservative 0; Mismatches 406; Indels 15; Gaps 4;

QY 11 ATGAGGATGTTACCATGTTGAAAGAGTTGGGTTTCAGAGAGGGGAGATATATATAA 70
DB 1 ATGAGGAGCTGCTATTGTGTAAGAGGCTGGCTGCACAAAGAGGAGTACATCAAG 60
QY 71 AACTGAGGCGCAAGATCTCTCTTTGAAGAGATGCTCATTTAGATATATAAGAG 130
DB 61 AACTGGCGGCGCAAGCTACTTCTCTCAAGATGATGCACTTATTTGGTACAAAGAG 120
QY 131 AAACCTCAAGATGTGATTTACCTTA--TCCCTCAACAACCTTTTCAATGCGAAATGC 187
DB 121 CGGCGCGAGATGTGAGCCACGATGAGGCTCCCTCAACAACCTTCTGTGGCGAGTGC 180
QY 188 CAGTTAATGAAACAGAACGACCAAGCAACCACTTATATAGATGTCTCCAGTGG 247
DB 181 CAGCTGATTAAGAGGAGGCGCCCGGCCCAACCTTATCATCTTCCGCTGCACTGG 240
QY 248 ACTACTGTATAGAGAACATTTATGATGATCTCCAGAGAAAGGAGAGATGAGCA 307
DB 241 ACCACGTGTCATGAGAGCACTTCCATGTGAGAGCTCTGAGAGCGGAGAGTGGACA 300
QY 308 GAACTATCCAGCTGTAGCAGACAGCTGCAGAGGCAAGAGAGAGATGAAATGT 367
DB 301 ACCGCGATCCAGACTGTGTGCTGACGCGCTCAAGAAACAGAGAGAGAGATGCACTTC 360
QY 368 AGTCCAACTTCAAAATGATATATAGAGAGAGAGATGGATGCTCTCAACCCAT 427
DB 361 CGGTGGGCTCACCCAGTACATCTAGAGGCGCTGAAGAGATGAGTGTCCCGCCAG 420
QY 428 C--ATMAAAGAAAGACAATGATGATTTTGACTATTTGAAACTAGAGTAAAGCACT 484
DB 421 CCCAAGCACCGCGTGACATGAACGAGTTTGAAGTACTGAAGCTGTGGCAAGGCACT 480
QY 485 TTTGGAAAGTATTTTGGTTGAGAGAGGCAAGTGGAAATACTATGCTATGAAAT 544
DB 481 TTGCGCAGAGTATCTGTGTGAAGAGAGGCGCACAGGCGCTACTACCCCATGAGATC 540
QY 545 CTGAAGAAAGATGCTATTATGCAAGATGAAAGTGGACAACAACCTTAAGTAAAGCAGA 604
DB 541 CTCAGAGAAAGATGCTATCTGTGCGCAAGAGAGAGTGGCCACACACTCACCGAAGCCG 600
QY 605 GTATTAAAGACAATAGACATCCCTTTTAACTCTTGAATATCTTCCAGACAAA 664
DB 601 GTCTGACAGAACTCCAGGACCCCTTCTCAAGCCCTGAAGTACTTTCCAGAGCCAG 660
QY 665 GACCGTTTGTGTTTGTGATGCAATATGTTAATGGGCGGAGCTGTTTTCATTTGTG 724
DB 661 GACCGCTCTGCTTGTGATGAGTACGCGCAACGCGGCGGAGTGTCTTCCACCTGTGC 720
QY 725 AAGAGAGCGGCTGTCTCTAGAGACGCGACAGTTTATGAGGAGAAATGCTCTGCG 784
DB 721 CGGGAACGTGTGTCTCTCGAGAGCGGCGCCGCTTATGAGCGCTGAGATGTGTAGCC 780
QY 785 TTGACTATCTACATTCGGAAGA--TTGTGTACCGTGAATCTCAAGTTGAGATCTTA 841

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DB 781 CTGACCTACCTGCACTCCGAGAAAGACGTGGTGTACCGGAGCTCAAGCTGAGAACCTC 840
QY 842 ATGCTGACAAAGATGGCCACATAAAATTAAGATTTTGAATTTTGGCAAAAGAGATC 901
DB 841 ATGCTGACAAAGAGAGGCGACATTAAGATCAACAGACTTGGGCTGTGACAGAGGAGATC 900
QY 902 ACAGATGACGACCATGAGATGACATTTCTGTGGCACTCCAGAAATATCTGACACAGAGTG 961
DB 901 AAGAGCGGTGACCATGAGATGAGCTTTTGGGCAACCTGAGTACTGGCCCCGAGGTG 960
QY 962 TTGAAGATTAATGACTATAGCCGAGACAGTGAATGAGTGGAGGCTGAGGAGTGTAT 1021
DB 961 CTGAGAGCAATGACTAGCGCGGTGAGAGCTGTGAGGAGCTGGGCTGTGTATGATAC 1020
QY 1022 GAAATGATGTGGAGAGTACTTTCTACACACGAGACATGAGAAATCTTTGATTA 1081
DB 1021 GAGATGATGTGGAGTGGCTGCTGCTCTTCAACACGAGACATGAGAAAGCTTTTGAAGCTC 1080
QY 1082 ATATTAAAGAAAGACATTAATTTTCTGAAACACTCTCTGATGCAAAATCATTTGCTT 1141
DB 1081 ATCTCATGAGAGATCCGCTTCCGCGACAGCTTGTGCTCGAGGCCAAGTCTTGCTT 1140
QY 1142 TCAGGCTCTTGATTAAGAGATCAAAATAAAGCCTTGTGAGAGACAGATGATCAAAA 1201
DB 1141 TCAGGCTGCTCAAGAAAGACCCCAAGAGAGGCTTGGCGGGGCTCCGAGAGCGCCAA 1200
QY 1202 GAAATTAAGACACAGTTTCTCTCTGAGATGAACCTGCAAGATGATATGATAAAG 1261
DB 1201 GAGATCATGACAGATCGCTTCTTTCGCGTATGATGTGGAGACAGTGTACGAGAAAG 1260
QY 1262 CTGTGACCTCTTTTAAACCTCAAGTAAATCTGAGACAGATGATGATTTGATGA 1321
DB 1261 CTCAGCCACCTTCAAGCCCAAGTCACTGAGAGCTGACACAGATTTTATGAG 1320
QY 1322 GAATTAAGCTCAGACTATTAATTAATTAACCACTGAAAAATATGATGAGATGATG 1381
DB 1321 GAGTCAAGGCCCAAGATATCAATCAACCACTGACCAA-----GATGACAGATG 1374
QY 1382 GACTGATGAGCAATGAGAGGCGCGCATTTCCCTCAATTTTCTACTCTGCAAG 1437
DB 1375 GAGTGTGTGACAGAGAGGCGGCCCACTTCCCGAGTTCTCTACTCGGCGAG 1430

RESULT 9
US-09-256-465-1
; Sequence 1, Application US/09256465
; Patent No. 6043090
; GENERAL INFORMATION:
; APPLICANT: Brect P. Monia
; APPLICANT: Lex M. Cowbert
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; FILE REFERENCE: RTS-0035
; CURRENT APPLICATION NUMBER: US/09/256,465
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (88)..(1533)
US-09-256-465-1

Query Match      42.5%; Score 658.2; DB 3; Length 1599;
Best Local Similarity 67.7%; Pred. No. 8,1e-188;
Matches 988; Conservative 0; Mismatches 453; Indels 18; Gaps 4;

QY 5 GTATCATGAGGAGATGTTACCATTTGTGAAAGAGTTGGGTTCAAGAGGGGAGAAATAT 64
DB 82 GCCACATGAATGAGATGTGTGTATCAAGAAAGAGCTGCTCAACAGCGTGTGATATAC 141

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QY ATAAAAAAGTGGAGCCCAAGATACCTTCTTTGAAGACAGATGGCTCATTCATAGGATAT 124
 DB ATCAAGACTGGAGCCACCGTACTCTCTCTGAAGACGACGCTCTTCATTTGGGTAC 201
 QY AAAGAGAACTTCAGATGTGATTTACCTTATCCCC--TCAACAATTTTGAAGTGGCA 181
 DB AAGAGAGGCGCCGAGGCCCCCTGATCAGACTCTACCCCCCTTAAACAACATCTTCGTAGCA 261
 QY AAATGCCATTTAATGAAGACAGACCAAGCCAAACATTTATATCAGATGTCTC 241
 DB GAATGCCAGCTGTATGAAGCCGAGAGGCCCCGACCCCAACATCTTGTTCATACCTCTGCTG 321
 QY CAGTGGACTCTCTTTAGAGAAACATTCATGTATCTCTCAAGAGAAAGGAAGAA 301
 DB CAGTGGACCAAGTTCATCGAAGACCTTCACGTGATTTCTCAAGCGAGAGAGAG 381
 QY TGGACAGAAAGCTATCCAGGCTGTAGCAGACAGCT-----GCAGAGCCAAAGAGAGAG 355
 DB TGGATGGGGGCATCCAGATGTGTGCCAAGGCTCAAGAGAGGCGGCCGAGGAGAGC 441
 QY AGAATGAATTTGTATCCAACTTCAAAATTGATTAATAGAGAGAGAGATGATGCC 415
 DB CCCATGAGACTACAAAGTGTGGCTCCCCAGTACTCTCCACGACTGAGAGATGGAAGTG 501
 QY TCTACAACCCAT---CATAAAGAAAGCAATGATGATTTGACTATTTGAACCTACTA 472
 DB GCGGTGACAGAGCAGCGGCTTAAGTGAATGATGATGATGATGATGATGATGATGATGAT 561
 QY GGTAAAGGCACTTTTGGGAAAGTATTTTGGTTTGAAGAGCAAGTGAAGAAATCTAT 532
 DB GCGAAGGAACTTTTGGCAAGTATCTGTGTGGGAGAGAGCCACTGGCCGCTACTAC 621
 QY GCTATGAAGTTTGAAGAAAGATCATTTTGAAGAGATGAAGTGAAGTGAAGTGAAGTGA 592
 DB GCATGAAGATCTTGGCAAGAGATCATTTTGAAGAGATGAAGTGAAGTGAAGTGAAGTGA 681
 QY ACTGAAGAGAGATTTAAAGAACATGACATCCCTTTTAAATCTTGAAGAAATTTCC 652
 DB ACCGAGAGCCGGGTCTCTCAAGAACACAGGACCCGTTCTCTCACTGGCTGAAGTATGCC 741
 QY TTCAGACAAAGAACCGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 712
 DB TTCACAAACCAAGACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 801
 QY TTCATTTTGTGAAGAGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 772
 DB TTCACCTGTCCGCGGAGCGTGTCTTCAAGAGAGGCGGCGGTTTATGTGTGAAG 861
 QY ATTGTCTGCGCTTGTGACTATCTACATCCGGAAGATTTGTATCCGTATCTCAAGTTG 832
 DB ATTGTCTGCGCTTGTGACTATCTGCACTCGCGGAGCGTGTATACCGGACATCAAGCTG 921
 QY GAGATCTAATGCTGCAAGAGATGCGCATATAAAATTCAGATTTTGAAGCTTTGCAAA 892
 DB GAAACCTATGCTGCAAGAGATGCGCATATAAAATTCAGATTTTGAAGCTTTGCAAA 961
 QY GAAAGGATCAAGATGACGACCATGAGAACATTTCTGTGCACTCTCAAGATTTCTGCA 952
 DB GAGGGGATCAGTACGCGGCGCACCATGAGAAACCTTCTGTGAGACCCGCGAGTACTGCGG 1041
 QY CCAAGAGTGTAAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1012
 DB CCAAGAGTGTAAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1101
 QY GTCATGTATGAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1072
 DB GTCATGTATGAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1161
 QY TTTGAATTAATTAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1132
 DB TTTGAATTAATTAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1221
 QY TCATTCCTTTCAAGGCTCTTGAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 1192

DB 1222 TCCCTCTGCTGGGCTGTGTTAAGAAAGACCCCAAGCAAGGCTTGTGGGGGCCACG 1281
 QY 1193 GATGCAAAAGAAATTAAGACACAGTTCTTCTGTGAGTAACTGCAAGATGTATAT 1252
 DB 1282 GATGCAAGAGAGATTAAGACACAGTTCTTCTGTGAGTAACTGCAAGATGTATAT 1341
 QY 1253 GATTAAGAGTGTACTCTCTTTTAACTCAAGTAACTGTGAGCAATACTAATAT 1312
 DB 1342 CAGAAAGACCTCTGACACCTTCAACCTCAGTACGATCCGAGGTGACACAAAGTAC 1401
 QY 1313 TTTGATGAAGAAATTAAGTCACTGAGTAACTTAAATTAACCACTGAAAAATTAAGTAC 1372
 DB 1402 TTGATGATGAATTTTACCGCCAGTCAATCAATCAACCTTCAACCGCTAT----- 1455
 QY 1373 GATGATGAGTCAATGAGCAATGAGAGAGGCGCGCATTTCTCTCAATTTCTTACTCT 1432
 DB 1456 GACAGCCTGGGCTTACTGAGGCTGACCAAGCCGACCACTTCCCGAGTTCTTCTACTCG 1515
 QY 1433 GCAAGTGAACGAGAAATAG 1451
 DB 1516 GCCAGCATCCGGAGTACG 1534

RESULT 10

US-09-167-322-3
 ; Sequence 3, Application US/09167322
 ; Patent No. 6365151
 ; GENERAL INFORMATION:
 ; APPLICANT: Allegheny University of the Health
 ; Sciences, Halpern, Michael S.
 ; England, James M.
 ; TITLE OF INVENTION: CANCER VACCINE
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Seidel, Gonda, Lavoigna & Monaco, P.C.
 ; STREET: Suite 1800, Two Penn Center Plaza
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/167,322
 ; FILING DATE: 07-Oct-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US97/00582
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Monaco, Daniel A.
 ; REGISTRATION NUMBER: 30,480
 ; REFERENCE/DOCKET NUMBER: 7933-33 PC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 568-8383
 ; TELEFAX: (215) 568-5549
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1599 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Query Match 42.5%; Score 658.2; DB 3; Length 1599;
 Best Local Similarity 67.7%; Pred. No. 8, 1e-188;
 Matches 988; Conservative 0; Mismatches 453; Indels 18; Gaps 4;

QY 5 GTTCATCATGAGCGATGTTACATTTGTGAAGAAGTTGGTTTCAGAGAGCGGAGATAT 64
 DB 82 GCCACATTAATGAGGTGTCTGTCATCAAGAAGGTGGCTCCAGAGGTTGATATAC 141
 QY 65 ATAAAAAATGAGGCGCAAGATATCTTCTTTGAGAGACAGATGGCTCATTCATAGATAT 124
 DB 142 ATCAAGACCTGAGGCGCAGGTACTTCTGCTGAAGAGCAGCGGCTCTTCAATGGGTAC 201
 QY 125 AAGAGAAACCTCAAGATGTGATTTACCTTATCCCC--TCAGCAACTTTTCAGTGGCA 181
 DB 202 AAGGAGAGGCCCCGAGGCCCCCTGATCAGACTTACCCCCCTTAAACAACTTCTTCCTAGCA 261
 QY 182 AATGCGCACTTAATGAAAAAGAGAGCAAGCAAGCCCAACATTTATTAATCAGATGTCTC 241
 DB 262 GAATGCGAGCTGATGAAAGCCAGAGAGCGCGGCGCAACCTTTGTCTATAGCTGCGCTG 321
 QY 242 CAGTGGACTACTGTTTATAGAGAGACATTTCTATGATATCTCAGAGAGAAAGGAGAA 301
 DB 322 CAGTGGACCAAGTCAATCAGAGAGACCTTCCAGTGAATTTCTCAGACGAGAGGAGAG 381
 QY 302 TGGACAGAGCTATCCAGGCTGTAGCAGACACT-----GAGAGGCGAAGAGAGAG 355
 DB 382 TGGATGCGGCGCCATCCAGATGTCGCAAGAGCTTAAGCAGGCGGCCCCAGCGAGAGAC 441
 QY 356 AGAATGAATTTGATGCCAATTCACAAATTTGATTAATATAGAGAGAGAGATGATGCC 415
 DB 442 CCATGGACTAAGAGTGTGGCTCCCGAGTGAATCTCCAGCACTGAGAGATGGAAGT 501
 QY 416 TCTCAACCCAT---CATAAAAAGAAAGACATGATGATTTGATTTGAAATCTACTA 472
 DB 502 GCGGTCAGAGAGGACGAGGCTAAAGGACATGAATGACCTTGAATCTCAATCCCTCT 561
 QY 473 GGTAAAGGACCTTTTGGAAAGTTATTTTGTGAGAGAGCAAGTGAATAATCTAT 532
 DB 562 GCGAAGGAGACCTTTGGCAAGTCACTCTGTCGCGGAGAAAGGCCACTGCGGCTACTAC 621
 QY 533 GGTATGAAGATTCTGAAGAAGAGTCAATTAATGCAAGATGAATGAGCAACAACCTCTA 592
 DB 622 GCATGAAGATCTGTGAAAGAGAGTCAATTCATGCAAGATGAATGAGTCTCAGACAGTC 681
 QY 593 ACTGAAGAGAGTATTAAGAAACATAGACATCCCTTTTAAATCTCTTGAATTTTC 652
 DB 682 ACCGAGAGCGGGGTCTCCAGAACACAGAGACCCCTTCTCCTCAGCTGAAGATGTC 741
 QY 653 TTCAGAGCAAAAGACCGTTTGTGTTTGTGATGAGAAATATGTAATGGGCGAGCTGTT 712
 DB 742 TTCAGAGCCCAAGACCGCTGTGCTTTGTGATGAGATATGCCAAGCGGAGTGAAGTTC 801
 QY 713 TTCATTTGTGAGAGAGCGGCTGTTCTGTAGAGACCGCAACGTTTCTATGGTGCAGA 772
 DB 802 TTCACCTGTCCCGGAGGCTGCTTCAAGAGAGACCGGCGGTTTATGTTGAGAG 861
 QY 773 ATTGTCTGCTGCTTGAATCTATCTACATTCGCGAAAGATTTGTGATCCGTATCTCAAGTTG 832
 DB 862 ATTGTCTGCTGCTTGAATCTATCTACATTCGCGGAGATGTTATCGCAATCAAGCTG 921
 QY 833 GAGATCTATGCTGAGCAAAAGTGGCAATTAATAATTAATGATTTTGAATTTGCAGAA 892
 DB 922 GAAAACTATGCTGAGCAAAAGTGGCCATCAATCAATCAATCTGATCTTGGCTCTGCAAA 981
 QY 893 GAAGGATCAAGATGACAGCCACCATGAAGACATTCGTGAGCACTCCAGAAATATCTGCA 952
 DB 982 GAGGGCATAGTGAAGCGGCGCACCATGAAGACCTTGTGGAGCCCCGAGTACCTGGG 1041
 QY 953 CCAAGGCTTTGAAGATTAATGATCTATGCGCGAGCACTGATGCTGGGCGCTAGGGGTT 1012
 DB 1042 CCGAGGCTCTGAGAGCAATGATGAGCCGCGGCTGAGTCTGAGGCGCTGAGGCTG 1101
 QY 1013 GTCATGTATGAATGATGTTGGGAGAGTTACCTTTTACACCAAGGACCATGAGAACTT 1072
 DB 1102 GTCATGTATGAATGATGTTGGGCGGCGCTGCTTTTACACCAAGGACCATGAGGCTT 1161
 QY 1073 TTTGAATTAATTAATGAAGACATTAATTTCTCGAACAACCTCTTCAAGATGCAGAA 1132

DB 1162 TTCGAGCTATCTCATGGAAGAGATCCGCTTCCCGCGACAGCTCAGCCCCGAGGCCAAG 1221
 QY 1133 TCATGCTTTCAAGGCTCTTGATTAAGATCCAAATTAAGCCTTGTGTGAGAGACCAAT 1192
 DB 1222 TCCTGCTTGTGAGGCTCTTAAAGAGACCCCAAGAGAGGCTGTGGGGGCGCCAGC 1281
 QY 1193 GATGCAAAAGAAATATGAGACACAGTTTCTTCTGTGAGTAACTGCAAGATGATAT 1252
 DB 1282 GATGCCAAGAGATCATGAGACAGGTTCTTCTCCAGATCAATGGCAGAGACCTGTGTC 1341
 QY 1253 GATAAAAAGCTTGAATCTCTTTTAAACCTCAAGTACATGTGAGACAGATATCTAGAT 1312
 DB 1342 CAGAAAGAGCTCTCCACCCCTTCAACCTCAGGTCAAGTCCGAGGTGAGACCAAGTAC 1401
 QY 1313 TTTGATGAAGATTTTACAGCTCAGCTATTAATAAACAACCTGAGAAAAATATGATGAG 1372
 DB 1402 TTCGATGATGAATTTTACCGCCAGTCCATCAATAACACACCCCTGAGCGCTAT----- 1455
 QY 1373 GATGTTATGAGACTGATGAGACATGAGAGAGGCGGCGCAATTTCCCTCAATTTTCTACTCT 1432
 DB 1456 GACAGCTGGGCTTACTGAGAGTGAACAGCGGAGCCACTTCCCAAGTTCTCTACTCG 1515
 QY 1433 GCAAGTGAACGAGATTAAG 1451
 DB 1516 GCCAGATCCGCGAGTGAAG 1534

RESULT 11
 US-09-023-655-1004
 ; Sequence 1004, Application US/09023655
 ; Patent No. 6607879
 ; GENERAL INFORMATION:
 ; APPLICANT: Cocks, Benjamin G.
 ; APPLICANT: Susan G. Stuart
 ; APPLICANT: Jeffrey J. Seilhamer
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
 ; NUMBER OF INVENTION: EXPRESSION
 ; NUMBER OF SEQUENCES: 1508
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 PORTER DRIVE
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/023,655
 ; FILING DATE: HERewith
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Zeller, Karen J.
 ; REGISTRATION NUMBER: 37,071
 ; REFERENCE/DOCKET NUMBER: PA-0001 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650) 855-0555
 ; TELEFAX: (650) 845-4166
 ; INFORMATION FOR SEQ ID NO: 1004:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1599 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:

LIBRARY: GENBANK
CLONE: 9178325
US-09-023-655-1004

Query Match 42.5%; Score 658.2; DB 4; Length 1599;
Best Local Similarity 67.7%; Pred. No. 8.1e-188;
Matches 988; Conservative 0; Mismatches 453; Indels 18; Gaps 4;

QY 5 GTTATCATGAGCATGTTACATTGTAAGAAAGTTGGGTTTCAAGAGAGGAGGAAATAT 64
DB 82 GCCACCATGAAATAGGTGTCTGTCATCAAGAAAGGCTGCTCCACAAGCTGTGTAAATC 141
QY 65 ATAAAAAAGTGGAGGCGCAAGATACCTCTTTGAAGAAGATGGCTCATTCATAGATAT 124
DB 142 ATAAAGCTGGAGGCGCAAGGTAATCTTCTCTGAAGAGCGAGCTCTTCATTTGGGTAC 201
QY 125 AAGAGAAACCTCAAGATGTGATTTACCTTATCCCC--TCAACAACCTTTTCAAGTGGCA 181
DB 202 AAGAGAGGCGCGAAGGCCCCGTGATCAAGACTCTACCCCCCTTAACAACCTTCTCGTAGCA 261
QY 182 AATGCCAGTTAATGAAGAAAGACGCAAGCCAAACATTTAATCAGATGCTC 241
DB 262 GATGCGAGCTGTATGAAGACCGAGAGGCGCGCAACCAACCTTTGTCAATACGCTGCTG 321
QY 242 CAGTGAAGTACTGTATPAGAGAAACATTTCAATGATATCTCAGAGAGAAAGGAGAA 301
DB 322 CAGTGAAGCAAGTCAATCGAGAGGACCTTTCAGTGAATTTCTCAAGCGAGAGAGAG 381
QY 302 TGGACAAAGCTATCCAGGCTGTAGCAGACGACT-----GCAGAGGCGAAGAGAGAG 355
DB 382 TGGATCGGGGCGATCCAGATGTCGCGCAACAGCTCAAGAGGCGGCGCCAGCGAGAGC 441
QY 356 AGAATGAATTTATGTCACACTTCAAAATTTAATAGAGAGAGAGAGATGCC 415
DB 442 CCCATGAGACTCAAGTGTGCTCCCCAGTAGCTCTCCACGACTAGAGAGATGAGT 501
QY 416 TCTACAACCAT---CATAAAAAGAAAGCAATGAATGATTTTGAATTTGAATCACTA 472
DB 502 GCGGTGAGCAAGGCGGCTTAAGTACCATTAATGACTTCGATCTCAATCTCAATCTCT 561
QY 473 GGTAAAGGCACTTTTGGGAAAGTTATTTTGTTCGAGAGAGGCAAGTGGAAATATCTAT 532
DB 562 GCGAAGGGAACCTTTGGCAAAAGTCATCTGTGCGGAGAGAGGCGCACTGGCGCTACTAC 621
QY 533 GCTATGAAGTTTGAAGAAAGATCATTTATTCGAAAGATGAAGTGGCACTCTA 592
DB 622 GCCATGAAGTCTTGGGAAAGGAAATCATTTGCCAAGATGAAGTGGCTCACACAGT 681
QY 593 ACTGAAGAGAGATTAATTAAGAACATAGACATCCCTTTTACATCCTTGAATAATTC 652
DB 682 ACCGAGGCGGGTCTCCAGAACACAGGACCCGTTCTCACTGCGTGAAGTATGCC 741
QY 653 TTCACAGCAAAAGACGTTTGTGTGTATGTAATATTTATGGGCGGAGCTGTT 712
DB 742 TTCACAGCCAGACGCGCTGTCTTGTGTATGTAAGTATCCAAACGCGGCTGAGCTGTC 801
QY 713 TTCATTTGTGAGAGAGCGGCTTCTCTGAGAGCCGACACGTTTCTATGCTGAGAA 772
DB 802 TTCACCTGTCCGCGAGCGTGTCTTCAAGAGAGGCGGCGCGGTTTATGCTGACAG 861
QY 773 ATTGTCTGCGCTTGAAGTATCTACATTCGGAAGATTTGTATACGTAATCTCAAGT 832
DB 862 ATTGTCTGCGCTTGAAGTATCTTGCACCTGCGGAGCGTGTATACGCGACATCAAGCT 921
QY 833 GAGAACTAATGCTGAGCAAAAGTGGCAATATAAATTTACAGATTTTGGACTTTGCA 892
DB 922 GAAACCTATGCTGAGCAAAAGTGGCAATCAAGATCACTGACTTTGGCTCTGCAAA 961
QY 893 GAAAGGATCAAGATGAGCGCACCATGAGACATTTCTGTGGCACTCCAGAAATCTGGCA 952
DB 982 GAGGGGATCAAGTACGCGGCGCACCATGAGAAACCTTCTGTGGAGCCCGCGAGTACTGGCG 1041
QY 953 CAGAGGTTTAAAGATTAATGACTATGCGGAGAGTACGATGAGGCGCTTAAGGCGTT 1012

DB 1042 CCTGAGGCTCTGAGAGCAATATGATGCGCCGCGCTGTGATGCTGAGGCGCTGTG 1101
QY 1013 GTTCATGATGAATGATGTTGTGGAGGTTACCTTTCTCAACACGAGACATGAGAACTT 1072
DB 1102 GTCATGTACGATGATGATGCGCGCGCTGCGCTTCTCAACACGAGACGAGCGCTTC 1161
QY 1073 TTTGAATTAATTAATGAGACATTAATTTCTCGAACAATCTCTTCAATGAGAA 1132
DB 1162 TTGAGACTCATCTCAATGAGAGATCGCTTCCGCGACGCTCAGCCGAGGCGAAG 1221
QY 1133 TCATTCCTTCAAGGCTCTTGAATTAAGATTCAAATTAACGCTTGTGAGAGACAGAT 1192
DB 1222 TCCCTGCTGCTGCGCTGCTTGAAGAGACCCCAAGACAGGCTTGTGTGGGCGCCAC 1281
QY 1193 GATGCAAAAGAAATTAAGAGACAGTTCCTCTGAGTAACCTGCAAGATGTATAT 1252
DB 1282 GATGCCAAGAGATGATGAGACAGGTTCTTCTCAGATCAACTGGCAGAGCGTGTG 1341
QY 1253 GATTAAGACCTGTATCTCTTTTAACCTCAAGTACATCTGAGACATATCTAGATAT 1312
DB 1342 CAGAAAGCTCTGCGACCTTCAACCTCAGGTCAAGTCAAGGTGACACAAAGTAC 1401
QY 1313 TTTGATGAAGATTTACAGCTCAGACTATTAACAATCAACCACTGAAATAATATGATGAG 1372
DB 1402 TTGATGATGAATTTACCGCCAGTTCATCAATCAACACCCCTGACCGCTAT----- 1455
QY 1373 GATGTATGAGCTGATGAGCAATGAGAGCGCGCGCATTTCTCAATTTTCTATCTCT 1432
DB 1456 GACAGCTGGCTTACTGTGAGCTGACGACGCGGACCACTTCCCGAGTTCCTACTCG 1515
QY 1433 GCAAGTGAACGAGATTAAG 1451
DB 1516 GCCAGCATCCGCGAGTGAAG 1534

RESULT 12
US-09-590-740-3
; Sequence 3, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-590-740-3

Query Match 39.1%; Score 604.4; DB 4; Length 1254;
Best Local Similarity 70.0%; Pred. No. 1.2e-171;
Matches 876; Conservative 0; Mismatches 361; Indels 15; Gaps 4;

QY 194 ATGAAGACGAGCGGCGCCGCGCAACCTTCAATCATCTGCTGCTGAGTGAACACT 253
DB 1 ATGAAGACGAGCGGCGCCGCGCAACCTTCAATCATCTGCTGCTGAGTGAACACT 60
QY 254 GTTATGAGAGAACTTTATGATGATCTCCAGAGAAAGGAGAAATGACAGAACT 313
DB 61 GTTCATGAGACGACCTTCAATGATGAGTCTCTGAGAGCGGAGAGTGAACACCGCC 120
QY 314 ATCCAGGCTGTAGCAGACGACTGCAAGGCGCAAGAGAGAGAAATGATTTGATCTCA 373
DB 121 ATCCAGACTGTGCGCGACGCTCAAGAGCGAGAGAGAGATGATCTTCCGCTG 180
QY 374 ACTTCAAAATTTGATTAATTAAGAGAGAGATGAGTGCCTTCAACACCATC--AT 430

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Db 181 GGCTCACCCAGCACAACCTCAGGGGCCGAAGATGAGGTGCTCTGGCCAAAGCCCAAG 240
Qy 431 AAAAAGAAAGCAATGAATGATTTTGAATTTGAATCTAAGTAAAGCACTTTTGG 490
Db 241 CACCGGCTACCAATGAACGATTTGAGTACCTGAACCTGTGGCAAGGCACTTTTGGC 300
Qy 491 AAAGTATTTTGGTGGAGAGAGCAAGTGAATAAATGATGCTATGAAATTTGAAG 550
Db 301 AAGGTATCTGTGTGAAGAGAAAGGCA---CAGGCTACTACGCCATGAAGATCTCAAG 357
Qy 551 AAAAGATGATTTATTCGAAAGAGTGAAGTGGCACACACTTAACTGAAAGCAGATTTA 610
Db 358 AAGGAAGTATCGTGGCCAAAGGACGAGTGGCCACACACTCAACGAGAACCGCTCCAG 417
Qy 611 AAGAACTATGACATCCCTTTTAAACATCCTTGAATATTCCTTCAGACAAAGCCGT 670
Db 418 CAGAACTCCAGGACACCCCTTCTCTACTCGCTGAAGTACTCTTTCAGACCCACGACGCG 477
Qy 671 TTGTGTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTCATTTGTGAGAGAG 730
Db 478 CTCTGCTTTGTCAATGAGTACGCAACGGGGGCGAGCTGTTTTCACCTGTCTCCGGAG 537
Qy 731 CCGGTGTTCTTGAAGACCGCACAGCTTCTATGTGCAAAATTTGCTCTGCTTGGAC 790
Db 538 CGGTGTTGCGCCAGGACCGGGCCCGCTTATGAGCGCTGAGATGTGTCAAGCCCTGAC 597
Qy 791 TATCTCATTTCCGGAAGA---TTGTATCCCGTATCTGAATGGAGATCTAATGCG 847
Db 598 TACCTGACCTCGAAGAAAGCTGTGTACCGGACCTCAAGTGAAGAACTCAATGCTG 657
Qy 848 GACAAAGATGCGCACATTAATAATTCAGATTTTGAATTTGCAAAAGAGATCAAGAT 907
Db 658 GACAAAGAGGGGACATTAAGATCAAGACTTGGGCTGTGCAAGAGAGGAGATCAAGAC 717
Qy 908 GCAACCACTGAAGACATTTCTGTGCACTCAAGATATCTGGCACCAAGGTTTGAAG 967
Db 718 GGTGCACCATGAAAGACTTTTGGCGGCAACCTGATACCTGCCCCCAGGGCTGGAG 777
Qy 968 GATATGATGATGCGGAGAGATGAGCTGTGGGGGCTGAGGGGTTGCTATGTAAGAG 1027
Db 778 GACAAATGATCAGCGCGGTGAGTGGAGTGGTGGGGCTGGGCTGTATGACGAGAG 837
Qy 1028 ATGTGTGGAGGTTTACCTTTCTACACACAGACCATGAGAACTTTTGAATTAATTA 1087
Db 838 ATGTGGGTGGCTGCTTCTTACACACAGACCATGAGAGCTTTTGAAGTCAATCCTC 897
Qy 1088 ATGGAAGACATTAATTTCTGGAACACTCTCTTCAAGATGCAAAATCATTTGCTTCA 1147
Db 898 ATGGAAGACATCGCTTCCCGGCAAGCTTGTGCTCCGAGGCCAAAGTCTTGTTCAGG 957
Qy 1148 CTCTTGATTAAGGATCAAAATTAAGCCTTGTGTGAGAGCAAGATGATGCAAAAGAAAT 1207
Db 958 CTGCTTAAGAAAGACCCCAAGCAGAGGCTTTGGGGGGCTCCGAGAGCCGCAAGAGATC 1017
Qy 1208 ATGAGACACAGTTTCTTCTCTGAGTAACTGGCAGATGATATGATTAATAAAGCTTGA 1267
Db 1018 ATGACACATCGCTTCTTACCGGTATCGTGTGCAACAGGTGACAGAAAGCTCAAC 1077
Qy 1268 CCTCTTTTAAACCTCAAGTACATGAGACAGATGATGATTTTGAAGAAATTT 1327
Db 1078 CCACCTTTCAAGCCCAAGGTCAGTGTGAGACAGACAGGATTTTATGAGAGGATTC 1137
Qy 1328 ACAGCTCAGACTTATCAATTAACACACACGTAATAATATGATGAGATGATGAGCTG 1387
Db 1138 ACAGCCCAATGATATCAATCAACACACCTGACCAA-----GATACACAGATGAGTGT 1191
Qy 1388 ATGACAAATGAGAGCGCGCATTTCCCTCAATTTCTACTCTGCAAGT 1439
Db 1192 GTGGAAGAGGAGGAGCGCCCACTTCCCAAGTTCTCTACTCGCCAGCG 1243
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RESULT 13

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US-09-474-922A-1
; Sequence 1, Application US/09474922A
; Patent No. 6187586
; GENERAL INFORMATION:
; APPLICANT: Bret P. Monia
; APPLICANT: Lex M. Cowert
; APPLICANT: Richard A. Roth
; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
; FILE REFERENCE: RTS-0036
; CURRENT APPLICATION NUMBER: US/09/474,922A
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 1
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-474-922A-1
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Query Match 26.1%; Score 403; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 3,5e-111;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 29 GTGAAGAAGGTTGGGTTTCAGAAAGGGGAGATATTAATAAACTGGAGGCCAAGATAC 88
Db 1 GTGAAGAAGGTTGGGTTTCAGAAAGGGGAGATATTAATAAACTGGAGGCCAAGATAC 60
Qy 89 TTCTCTTTGAAGACAGATGGCTCATTCATGAGTATTAAGAGAACTCAAGATGTGAT 148
Db 61 TTCTCTTTGAAGACAGATGGCTCATTCATGAGTATTAAGAGAACTCAAGATGTGAT 120
Qy 149 TTACCTTATCCCTCAACAACTTTTCAGTGGCAAAATGCCAGTTAATGAAAAAGAGCA 208
Db 121 TTACCTTATCCCTCAACAACTTTTCAGTGGCAAAATGCCAGTTAATGAAAAAGAGCA 180
Qy 209 CCAAGCCCAACACATTTATATCAAGTGTCTCCAGTGAATCTGTTATGAGAGACA 268
Db 181 CCAAGCCCAACACATTTATATCAAGTGTCTCCAGTGAATCTGTTATGAGAGACA 240
Qy 269 TTTCAATGATATATCCAGAGGAAGGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 328
Db 241 TTTCAATGATATATCCAGAGGAAGGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 300
Qy 339 GACAGATGCGAGGCAAGAGAGAGAGATGAATGATGATGATGATGATGATGATGATGAT 388
Db 301 GACAGATGCGAGGCAAGAGAGAGAGATGAATGATGATGATGATGATGATGATGATGAT 360
Qy 389 AATATGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 431
Db 361 AATATGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 403
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RESULT 14
US-09-474-922A-2
; Sequence 2, Application US/09474922A
; Patent No. 6187586
; GENERAL INFORMATION:
; APPLICANT: Bret P. Monia
; APPLICANT: Lex M. Cowert
; APPLICANT: Richard A. Roth
; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
; FILE REFERENCE: RTS-0036
; CURRENT APPLICATION NUMBER: US/09/474,922A
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 2
; LENGTH: 387
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-474-922A-2
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Query Match 24.8%; Score 383.8; DB 3; Length 387;
Best Local Similarity 99.5%; Pred. No. 2,1e-105;
Matches 385; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy	912	TTGACTATGAGCGAGCAGTAACTCTGAGGGGCTTAGGGGTTGCTATGTATGAATGAGCT	1033
Db	1	ATGACTATAGCCGAGCAGTAACTCTGAGGGGCTTAGGGGTTGCTATGTATGAATGAGCT	60
Qy	1032	GTGGAGAGTTACCTTTCTACAAACCGAGCAGATGAGAAACTTTTGAATTAATTAATGAG	1093H
Db	61	GTGGAGAGTTACCTTTCTACAAACCGAGCAGATGAGAAACTTTTGAATTAATTAATGAG	120
Qy	1092	AAGACATTAAATTTCTTGAACTCTCTTCAGATGCAAAATCATTCCTTCAAGGCTCT	1151H
Db	121	AAGACATTAAATTTCTTGAACTCTCTTCAGATGCAAAATCATTCCTTCAAGGCTCT	180
Qy	1152	TGATTAAGAGATCCAAATTAACGCCCTTGCTGAGAGCCAGATGATGCCAAAGAAATATGAC	1211H
Db	181	TGATTAAGAGATCCAAATTAACGCCCTTGCTGAGAGCCAGATGATGCCAAAGAAATATGAC	240
Qy	1212	GACACAGTTTCTCTCTGAGATTAACCTGGCAAGATGTATGATTAATAAAGCTTGACTCTC	1273H
Db	241	GACACAGTTTCTCTCTGAGATTAACCTGGCAAGATGTATGATTAATAAAGCTTGACTCTC	300
Qy	1272	CTTTTAAACCTCAAGTAACTCTGAGACAGATCTAGATATTTTGATGAAGAATTTACAG	1333H
Db	301	CTCTTAAACCTCAAGTAACTCTGAGACAGATCTAGATATTTTGATGAAGAATTTACAG	360
Qy	1332	CTCAGACTATTAACAATAACACCACTG	1358H
Db	361	CTCAGACTATTAACAATAACACCACTG	387

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RESULT 15
US-09-949-016-1676
; Sequence 1676, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1676
; LENGTH: 2239
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1676

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	Query Match	Similarity	17.2%	Score	266.4	DB	4	Length	2239	
	Best Local	Similarity	56.1%	Pred	NC	1.7e-69				
	Matches	523	Conservative	0	Mismatches	406	Indels	3	Gaps	1
Qy	435	GAAGACATGATGATTTTGA	CTATTGAA	CTACTGATGAAGCACTTTTGGGAAAG	494					
Db	807	GGATGAAACGTGCCCATTTTAACTTCTTAATGGTGCTGGGGAAAGGCAAGCTTTGGCAAG	866							
Qy	495	TTATTTGGTTCGAGAGAGGCAATGTGAAAAATACATGCTATGATGAAGTTCGAAAGAAG	554							
Db	867	TCATGCTTTCAGAAAGAAAGGCAAGATGAGCTTAATGCTGTGAAGATCTGAAAGAAG	926							
Qy	555	AAGCATATTATTCGAAAGATGAAGGCAACACTTAACGTAAAGCAGATATT--AA	611							
Db	927	ACGTTGTATCCAAATGATGACGGGAGTGCACTATGATGAGAAAGCGGGTGTGGCCC	986							
Qy	612	AGAACACTGACATCCCTTTTAAATCATCTCTGAAATATTTCTTCGACAAAGACGGT	671							

Db	987	TGCCCCGGAACCGCCCTCTCCTGACCCAGCTCCACTCTCCTGTTCCAAACCATGGACCGCC	1046
Qy	672	TGTGTTTTGTGANGGAANAATGTTAATGGGGGGCGAGCTGTTTTTCATTGTTGTCCGAGAGC	731
Db	1047	TGTACTTTGTGATGSAATACGTGAATGGGGGGCGACCTCATGTATCATCATCCAGCAAGTGC	1106
Qy	732	GGGTGTTCTCGAAGACCGCACACGTTTCTAATGATGAGAAATGTCTCTGCTTGAGACT	791
Db	1107	GCCGGTTCAAGAGACCCCATGCTGTATTTTACGTGACGAANAATGGCCATCGTCTGTCTT	1166
Qy	792	ATCTACATTCGGGAAAGATTGTGTACCGGTGATCTCAAGTTGGAGAACTTAATGCTGACA	851
Db	1167	TCTTACAGAGTAAGGCGATCATTTACCGTACCTAAACCTTGACAAGTGAATGCTGATTT	1226
Qy	852	AAGATGGCCACATNAATAATTACAGATTTTGGACTTTGSCAAAGAAGGAGTCAAGATGACG	911
Db	1227	CTGAGGGGACATCATAGATTGGCCGATTTTGGCATGTGTAAAGAAAAATCATCTGGGATGGG	1286
Qy	912	CCACCATGAGAGACATTTCTGTGGCATCTCCAGAAATCTGTGGACCCAGAGGTGTAGAAATA	971
Db	1287	TGACAACCCMAACACTTCTGTGGCATCTCCAGACTACATCGCCCCCGAGATTAATGCTTATC	1346
Qy	972	ATGACTATGGCCGAGCAGTAGACTGATGAGGGGCCCTAGGGGTTGTGATGATGAATGATGT	1031
Db	1347	AGCCCTATGGSAATCCGTGGATTTGGTGGGCAATTTGGAGTCTGCTTAATGAANAATGTTGG	1406
Qy	1032	GTGGGAGGTTACCTTTCTTACACACAGGACCATGAGAACTTTTGAATTAATTAATG	1091
Db	1407	CTGGGCAAGGACCTTTTGAAGGGGAGATGAAAGTAGAATCTTCCATTCATCATATGAAAC	1466
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Db	1587	AGCATGCAATTTTCCGGTATATTGATTTGGGAGAACTTGAACGAAAGAAATCCAGCCCC	1646
Qy	1272	CTTTTAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTTGTATGAAGAATTTTACG	1331
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Job time : 302 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: April 13, 2005, 04:09:48 ; Search time 4784 Seconds
(without alignments)
1961.790 Million cell updates/sec

Title: US-09-869-079b-1

Perfect score: 1547

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5622541 seqs, 303355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1537	99.4	2811	15	US-10-324-985A-4
2	1537	99.4	2811	19	US-10-753-267-107
3	1364.8	88.2	1570	10	US-09-526-043-1
4	1364.8	88.2	1570	17	US-10-394-568-1
5	843	54.5	2410	9	US-09-771-161A-66
6	751.4	48.6	2626	15	US-10-324-985A-1
7	751.4	48.6	2626	18	US-10-713-678-5
8	751.4	48.6	2626	19	US-10-735-461-20
9	722.4	46.7	2729	19	US-10-895-225A-56
10	722.4	46.7	2729	19	US-10-895-225A-36
11	722.4	46.7	2978	10	US-09-955-999-43

12	721.2	46.6	2184	14	US-10-072-036-138	Sequence 138, App
13	719.2	46.5	2610	9	US-09-970-000-3	Sequence 3, App1
14	719.2	46.5	2610	17	US-10-388-263-329	Sequence 329, App
15	719.2	46.5	2610	17	US-10-641-643-1206	Sequence 1206, App
16	719.2	46.5	2610	18	US-10-713-678-1	Sequence 1, App1
17	719.2	46.5	2610	19	US-10-735-461-22	Sequence 22, App1
18	719.2	46.5	2610	19	US-10-823-433-3	Sequence 3, App1
19	716.4	46.3	2181	14	US-10-072-036-70	Sequence 70, App1
20	682.2	44.1	1122	18	US-10-322-281-412	Sequence 412, App
21	682.2	44.1	1741	15	US-10-324-985A-2	Sequence 2, App1
22	682.2	44.1	1741	15	US-10-735-461-21	Sequence 21, App1
23	682.2	44.1	3010	19	US-10-895-225A-57	Sequence 57, App1
24	658.2	42.5	1599	15	US-10-324-985A-3	Sequence 3, App1
25	658.2	42.5	1599	17	US-10-641-643-1004	Sequence 1004, App
26	658.2	42.5	1715	15	US-10-007-926A-254	Sequence 254, App
27	658.2	42.5	1715	19	US-10-735-461-23	Sequence 23, App1
28	655.2	42.4	2562	18	US-10-322-281-415	Sequence 415, App
29	604.4	39.1	1254	18	US-10-713-678-3	Sequence 3, App1
30	586.2	37.9	1140	15	US-10-324-985A-5	Sequence 5, App1
31	572	37.0	968	9	US-09-771-161A-65	Sequence 65, App1
32	515.8	33.3	1854	14	US-10-198-846-984	Sequence 984, App
33	457.2	29.6	3712	18	US-10-473-939-7	Sequence 7, App1
34	443.6	28.7	879	17	US-10-424-539-21419	Sequence 21419, App
35	403	26.1	403	15	US-10-168-771-1	Sequence 1, App1
36	383.8	24.8	387	15	US-10-168-771-2	Sequence 2, App1
37	380.6	24.6	758	9	US-09-910-943-677	Sequence 677, App
38	274.2	17.7	2391	17	US-10-172-118-1423	Sequence 1423, App
39	274.2	17.7	2391	17	US-10-295-027-115	Sequence 115, App
40	274.2	17.7	2391	17	US-10-342-887-1423	Sequence 1423, App
41	274.2	17.7	2391	18	US-10-737-450-3	Sequence 3, App1
42	274.2	17.7	2512	9	US-09-784-249-1	Sequence 1, App1
43	274.2	17.7	2572	11	US-09-764-875-302	Sequence 302, App
44	274.2	17.7	2702	11	US-09-764-875-148	Sequence 148, App
45	272.6	17.6	3884	18	US-10-755-889-41	Sequence 41, App1

ALIGNMENTS

RESULT 1
US-10-324-985A-4
; Sequence 4, Application US/10324985A
; Publication No. US20030144204A1
; GENERAL INFORMATION:
; APPLICANT: Spencer, David
; TITLE OF INVENTION: Akt-biased Inducible Survival Switch for Gene Therapy
; FILE REFERENCE: P02248US1/10106761
; CURRENT APPLICATION NUMBER: US/10/324,985A
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,155
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 2811
; TYPE: DNA
; ORGANISM: human
US-10-324-985A-4

Query Match 99.4%; Score 1537; DB 15; Length 2811;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 71 AACTGAGGCCCAAGATCTCTTTTGAAGACAGATGCTCATTTATAGATATATAGG 130
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RESULT 2
US-10-753-267-107
; Sequence 107, Application US/10753267
; Publication No. US20050037946A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Stagliano, Nancy E.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Donoghue, Mary A.
; APPLICANT: Rodriguez-May, Amelie
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,
; TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,
; TITLE OF INVENTION: 9380, 2569654, 33556, 53656, 44443, 32612, 10671, 261,
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 15319, 43969, 8921, 8993, 955,
; TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,
; FILE REFERENCE: MP103-0031R0NMNM
; CURRENT APPLICATION NUMBER: US/10/753,267
; CURRENT FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 60/439,683
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/445,216
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,036
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/454,189
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/457,541
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/466,411
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/469,041
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/477,414
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/478,560
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/489,772
; PRIOR FILING DATE: 2003-07-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
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; LENGTH: 2811
; TYPE: DNA

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 LOCATION: (1) ... (1440)
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 QY 791 TATCTACATTCGGAAGATTTGTACCGTATCTCAAGTTGAGATCTAATGCTGAC 850
 DB 781 TATCTACATTCGGAAGATTTGTGTACCGTATCTCAAGTTGAGATCTAATGCTGAC 840
 QY 851 AAAGATGCGCAATATAAATTAAGATTTTGAATTTGCAAAAGAGATCAAGATGA 910
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 DB 901 GCCACATGAGACATTTCTGTGACATCCAGATATCTGACACAGAGGTGTAGAGAT 960

QY 971 AATGACTATGCGGACAGCTAGACTGTGCGGCTTAGGGCTTGATGATGAATGANG 1030
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 DB 1441 GTCTCTTCAATCTGCTACTTCACTGATCTTCAATTTTATTAAGTAAATGATCTG 1500
 QY 1511 ACATCACCGCTCTAGCTTTTACATGACATGACAGGGGCA 1547
 DB 1501 ACATCACCGCTCTAGCTTTTACATGACATGACAGGGGCA 1537

RESULT 3

US-09-526-043-1
 ; Sequence 1, Application US/09526043
 ; Publication No. US20030100049A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Guo, Kun
 ; APPLICANT: Pagnoni, Marco
 ; APPLICANT: Clark, Kenneth
 ; APPLICANT: Ivaschenko, Yuri
 ; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
 ; FILE REFERENCE: A3278A-US
 ; CURRENT APPLICATION NUMBER: US/09/526,043
 ; EARLIER FILING DATE: 2000-03-14
 ; EARLIER APPLICATION NUMBER: 60/125,108
 ; EARLIER FILING DATE: 1999-03-19
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 1570
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (126) .. (1523)
 US-09-526-043-1

Query Match 88.2%; Score 1364.8; DB 10; Length 1570;
 Best Local Similarity 98.4%; Pred. No. 0;
 Matches 1378; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
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Db      176 AATATATAAAAAAGTGGAGGCAAGATACCTCTTTTGAAGACAGATGGGCTCATTAAG 235
Qy      121 AATATAAGAAAGCTCAGATGTGATTTACCTTATCCCTCAACAATTTCAGTGGC 180
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Qy      241 CCAAGGCACTACTGTTATAGAGAGAACATTTGATGATGATCTCCAGAGAAAGGAAA 300
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Qy      301 ATGACAGAGAGCTATCAGAGCTGTAGACAGACTGACAGAGCAAGAGAGAGAGAT 360
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Qy      421 AACCCATCTTAAAGAAAGCAATGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 480
Db      536 AACCCATCTTAAAGAAAGCAATGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 595
Qy      481 CACTTTGGGAAAGTATTTGGTTGAGAGAGAGCAAGTGGAAATATATATATATATATATAT 540
Db      596 CACTTTGGGAAAGTATTTGGTTGAGAGAGAGCAAGTGGAAATATATATATATATATATAT 655
Qy      541 GATTCGAGAAAGAAAGTATTTGCAAAAGATGAGTGAAGTGGCAACACTCTTAACTGAAG 600
Db      656 GATTCGAGAAAGAAAGTATTTGCAAAAGATGAGTGAAGTGGCAACACTCTTAACTGAAG 715
Qy      601 CAGAGATTTAAAGAACATGACATCCCTTTTAAATCCTTTGAAATATTTCTTCCAGAC 660
Db      716 CAGAGATTTAAAGAACATGACATCCCTTTTAAATCCTTTGAAATATTTCTTCCAGAC 775
Qy      661 AAAAGACGTTTGTGTTTGTGATGATGATGTTAATGGGGCGAGCTGTTTTCCATT 720
Db      776 AAAAGACGTTTGTGTTTGTGATGATGATGTTAATGGGGCGAGCTGTTTTCCATT 835
Qy      721 GTGAGAGAGCGGGTGTCTGTAGAGACCGCAACGTTTCTATGTGTGAGAAATGTCTC 780
Db      836 GTGAGAGAGCGGGTGTCTGTAGAGACCGCAACGTTTCTATGTGTGAGAAATGTCTC 895
Qy      781 TGCCTTGGACTATCTATCATTTCCGGAAAGATGTGTACCGTGTATCTCAATTTGAGATCT 840
Db      896 TGCCTTGGACTATCTATCATTTCCGGAAAGATGTGTACCGTGTATCTCAATTTGAGATCT 955
Qy      841 AATGTGACAAAGATGCGCACATAAAATTAACAGATTTTGAAGCTTTGCAAAAGAGAT 900
Db      956 AATGTGACAAAGATGCGCACATAAAATTAACAGATTTTGAAGCTTTGCAAAAGAGAT 1015
Qy      901 CACAGATGACCAACCATGAAGACATTTGTGTGCACTCCAGAAATATCTGGCACAGAGGT 960
Db      1016 CACAGATGACCAACCATGAAGACATTTGTGTGCACTCCAGAAATATCTGGCACAGAGGT 1075
Qy      961 GTTAGAAGTAATGATATAGTGGCGAGCACTGCTGTGGGCTCTAGAGGCTGTCTATGTA 1020
Db      1076 GTTAGAAGTAATGATATAGTGGCGAGCACTGCTGTGGGCTCTAGAGGCTGTCTATGTA 1135
Qy      1021 TGAATATGATGTGGAGGTTACCTTTCTACAACAGAGCACTATGAGAAATCTTTTGAAT 1080
Db      1136 TGAATATGATGTGGAGGTTACCTTTCTACAACAGAGCACTATGAGAAATCTTTTGAAT 1195
Qy      1081 AATATTTATGAGAGACATTTAAATTTCTGTGAACACTCTCTTCAAGATGCAAAATCATTTGCT 1140

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Db      1196 AATATTTATGAGAGACATTTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTTGCT 1255
Qy      1141 TTCAGGGCTCTTGAATTAAGATTCGAATTAACGCTTGTGGAGGACAGATGATGCAA 1200
Db      1256 TTCAGGGCTCTTGAATTAAGATTCGAATTAACGCTTGTGGAGGACAGATGATGCAA 1315
Qy      1201 AGAAATTAATGAGACAGATTTCTTCTGTGAGTAAATGCGAAGATGATATGATTA 1260
Db      1316 AGAAATTAATGAGACAGATTTCTTCTGTGAGTAAATGCGAAGATGATATGATTA 1375
Qy      1261 GCTTGACTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATTAATTTGATGTA 1320
Db      1376 GCTTGACTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATTAATTTGATGTA 1435
Qy      1321 AGAATTTACAGCTGAGCTATTAACAATTAACCACTGAAAATATGATGAGATGAT 1380
Db      1436 AGAATTTACAGCTGAGCTATTAACAATTAACCACTGAAAATATGATGAGATGAT 1495
Qy      1381 GCACTGACATGACAAATGAGA 1400
Db      1496 TGGCATGCTGGGTAACTGGA 1515

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RESULT 4
US-10-394-568-1
; Sequence 1, Application US/10394568
; Publication No. US20040002136A1
; GENERAL INFORMATION:
; APPLICANT: GUO, KUN
; APPLICANT: IVASHCHENKO, YURI
; APPLICANT: CLARK, KENNETH L.
; TITLE OF INVENTION: INDUCTION OF VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
; FILE REFERENCE: A3399WO
; CURRENT APPLICATION NUMBER: US/10/394,568
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/584,938
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (126)..(1523)
US-10-394-568-1

```

Query Match 88.2%; Score 1364.8; DB 17; Length 1570;
 Beef Local Similarity 98.4%; Pred. No. 0;
 Matches 1378; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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Qy      1 GGGAGTCATCATGAGGATGTTACCATGTGAAAAGAGGTGGGTTGAGAAAGGGGAGA 60
Db      116 GGGAGTCATCATGAGGATGTTACCATGTGAAAAGAGGTGGGTTGAGAAAGGGGAGA 175
Qy      61 AATATATAAAAAAGTGGAGGCAAGATACCTCTTTTGAAGACAGATGGCTCATTAAG 120
Db      176 AATATATAAAAAAGTGGAGGCAAGATACCTCTTTTGAAGACAGATGGGCTCATTAAG 235
Qy      121 AATATAAGAAAGCTCAGATGTGATTTACCTTATCCCTCAACAATTTCAGTGGC 180
Db      236 AATATAAGAAAGCTCAGATGTGATTTACCTTATCCCTCAACAATTTCAGTGGC 295
Qy      181 AAAATGCCAGTTAATGAAAAAGAACGACCAAAAGCCAAACACATTTATATCAGATGCT 240
Db      296 AAAATGCCAGTTAATGAAAAAGAACGACCAAAAGCCAAACACATTTATATCAGATGCT 355
Qy      241 CCAAGGCACTACTGTTATAGAGAGAACATTTGATGATGATCTCCAGAGAAAGGAAA 300
Db      356 CCAAGGCACTACTGTTATAGAGAGAACATTTGATGATGATCTCCAGAGAAAGGAAA 415

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QY 301 ATGACAGAGACTATCCAGGCTGTAGACAGACTGCAGAGGCAAGAGAGAGAAAT 360
DB 416 ATGGAGAGAGACTATCAGGCTGTAGACAGACTGCAGAGGCAAGAGAGAGAAAT 475
QY 361 GAATGTAGTCCAACTTCCAAATTTATATATAGAGAGAGAGATGGATGCTCTAC 420
DB 476 GAATGTAGTCCAACTTCCAAATTTATATATAGAGAGAGAGATGGATGCTCTAC 535
QY 421 AACCCATCTTAAAGAGAGAGAGATGATGATTTTGAATTTGAATTTGAATTTGA 480
DB 536 AACCCATCTTAAAGAGAGAGAGATGATGATTTTGAATTTGAATTTGAATTTGA 595
QY 481 CACTTTGGGAAAGTATTTGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 596 CACTTTGGGAAAGTATTTGGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 655
QY 541 GATTTGAG 600
DB 656 GATTTGAG 715
QY 601 CAGAGATTTAAAG 660
DB 716 CAGAGATTTAAAG 775
QY 661 AAAAGACGTTTGTGTTTGTGATGAGATATGTTAATGGGGGAGAGAGAGAGAGAG 720
DB 776 AAAAGACGTTTGTGTTTGTGATGAGATATGTTAATGGGGGAGAGAGAGAGAGAG 835
QY 721 GTGAG 780
DB 836 GTGAG 895
QY 781 TGCCTTGAAGTATCTAATCTCCGAAAGATTTGTAACCGTATCTCAAGTTGAGATCT 840
DB 896 TGCCTTGAAGTATCTAATCTCCGAAAGATTTGTAACCGTATCTCAAGTTGAGATCT 955
QY 841 AATGCTGAGCAAAAG 900
DB 956 AATGCTGAGCAAAAG 1015
QY 901 CACAGATGAG 960
DB 1016 CACAGATGAG 1075
QY 961 GTTAGAAGATATGACTATGAGCCGAGCAGTGAATGCTGAGGAGCTTATGAGTAT 1020
DB 1076 GTTAGAAGATATGACTATGAGCCGAGCAGTGAATGCTGAGGAGCTTATGAGTAT 1135
QY 1021 TGAAGATGATGTGAG 1080
DB 1136 TGAAGATGATGTGAG 1195
QY 1081 AATATTAATGAG 1140
DB 1196 AATATTAATGAG 1255
QY 1141 TTCAGGAGCTCTGTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1256 TTCAGGAGCTCTGTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1315
QY 1201 AGAAATTAAG 1260
DB 1316 AGAAATTAAG 1375
QY 1261 GCTTGTACCTCTTTTAACTCAAGTAAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
DB 1376 GCTTGTACCTCTTTTAACTCAAGTAAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1435
QY 1321 AGAATTAAG 1380
DB 1436 AGAATTAAG 1495
QY 1381 GAGACTGATGAG 1400

DB 1496 TGCATGCTGGGTAATCTGGA 1515

RESULT 5
US-09-771-161A-66
; Sequence 66, Application US/09771161A
; Patent No. US2002010811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; LENGTH: 2410
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-771-161A-66

Query Match 54.5%; Score 843; DB 9; Length 2410;
Best Local Similarity 100.0%; Pred. No. 5.9e-215;
Matches 843; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 705 ACCTGTTTTCATTTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 764
DB 312 ACCTGTTTTCATTTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 371
QY 765 GTGCAAGAAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 824
DB 372 GTGCAAGAAATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 431
QY 825 TCAAGTGGAGAGATCTAATGCTGCAAAAGATGGCCACATTAATAATTCAGATTTTGGAC 884
DB 432 TCAAGTGGAGAGATCTAATGCTGCAAAAGATGGCCACATTAATAATTCAGATTTTGGAC 491
QY 885 TTTGCAAGAGAGAGATCAGATGCAAGCCACATGAAGATTTCTGTGCACTCCAGAAAT 944
DB 492 TTTGCAAGAGAGAGATCAGATGCAAGCCACATGAAGATTTCTGTGCACTCCAGAAAT 551
QY 945 ATCTGCAACAGAGGTTTGAAGATTAATGACTATGAGCCGAGCAGTGAATGCTGAGGAGC 1004
DB 552 ATCTGCAACAGAGGTTTGAAGATTAATGACTATGAGCCGAGCAGTGAATGCTGAGGAGC 611
QY 1005 TAGGGGTTGTCAATGATGAATGATGTGAGAGGTTACCTTTCTTCAACAACAGAGACATG 1064
DB 612 TAGGGGTTGTCAATGATGAATGATGTGAGAGGTTACCTTTCTTCAACAACAGAGACATG 671
QY 1065 AGAAACTTTTGAATTAATTAATTAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1124
DB 672 AGAAACTTTTGAATTAATTAATTAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 731
QY 1125 ATGCAAAATCAATGCTTTTCAAGGAGCTTGAATTAAGAGATCAAAATTAAGAGCTTGGAGAG 1184
DB 732 ATGCAAAATCAATGCTTTTCAAGGAGCTTGAATTAAGAGATCAAAATTAAGAGCTTGGAGAG 791
QY 1185 GACAGAGATGATCAAAAG 1244
DB 792 GACAGAGATGATCAAAAG 851
QY 1245 ATGTATATGATTAAG 1304
DB 852 ATGTATATGATTAAG 911
QY 1305 CTAGATATTTTATGAAG 1364

Db 912 CTAGATATTTTATGTAAGAAATTTACAGCTCAGACTTATCAATTAACACCACTGAAAAAT 971
Qy 1365 AAGTAAGAGATGTATGATCTGATGAGACAAATGAGAGGGCGCGATTTCCCTCAATTTT 1424
Db 972 AATGAAGAGATGTATGATCTGATGAGACAAATGAGAGGGCGCGATTTCCCTCAATTTT 1031
Qy 1425 CCTACTCTGCAAGTGAAGAGATAGTCTCTTTCACTTCTGCTACTTCACTGTCAATCTTC 1484
Db 1032 CCTACTCTGCAAGTGAAGAGATAGTCTCTTTCACTTCTGCTACTTCACTGTCAATCTTC 1091
Qy 1485 AATTTATTTACTGAAAAATGATTCCTGACATCAACAGTCTAGCTCTTACATAGAGGG 1544
Db 1092 AATTTATTTACTGAAAAATGATTCCTGACATCAACAGTCTAGCTCTTACATAGAGGG 1151
Qy 1545 GCA 1547
Db 1152 GCA 1154

RESULT 6
US-10-324-985A-1
Sequence 1, Application US/10324985A
Publication No. US20030144204A1
GENERAL INFORMATION:
APPLICANT: Spencer, David
TITLE OF INVENTION: Akt-based Inducible Survival Switch for Gene Therapy
FILE REFERENCE: P02248US1/10106761
CURRENT APPLICATION NUMBER: US/10/324,985A
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US 60/342,155
PRIOR FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 2626
TYPE: DNA
ORGANISM: mouse
US-10-324-985A-1

Query Match 48.6%; Score 751.4; DB 15; Length 2626;
Best Local Similarity 71.8%; Pred. No. 2.3e-190;
Matches 1044; Conservative 0; Mismatches 396; Indels 15; Gaps 4;

Qy 8 ATCATGAGGATGTATTCATTTGTAAGAAAGTGGCTCAGAAAGGGAGAAATATATA 67
Db 281 ACCATGATGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 340
Qy 68 AAAAAGCTGAGGCGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 127
Db 341 AAAAAGCTGAGGCGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 400
Qy 128 GAGAAAGCTGAGGCGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 184
Db 401 GAGAGGCTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 460
Qy 185 TSCGATTTATGAAAAAG 244
Db 461 TSCGATTTATGAAAAAG 520
Qy 245 TGAAGTACTGTATAGAGAAATTTTATGATGATGATGATGATGATGATGATGATGATGAT 304
Db 521 TGAAGTACTGTATAGAGAAATTTTATGATGATGATGATGATGATGATGATGATGATGAT 580
Qy 305 AAGAAAGCTATCCAGGCTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 364
Db 581 GCAACGCGCATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 640
Qy 365 TGAAGTACTGTATAGAGAAATTTTATGATGATGATGATGATGATGATGATGATGATGAT 424
Db 641 TCCGATTCAGGCTCAGCCAGTGAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 700
Qy 425 CATC--ATMAAAGAAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 481

Db 701 AAGCCAAAGCACCGTGTGACCATGAAACGATTTGATGATGATGATGATGATGATGATGAT 760
Qy 482 ACTTTTGGAAAAATATTTTGGTTGGAGAGAAAGCAATGAGAAAAATATCTATGATGAA 541
Db 761 ACCTTTGGAAAAATATTTTGGTTGGAGAGAAAGCAATGAGAAAAATATCTATGATGAA 820
Qy 542 ATTCTGAAGAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 601
Db 821 ATCTCTAAGAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 880
Qy 602 AAGATATTTAAAGACATGACATGATGATGATGATGATGATGATGATGATGATGATGAT 661
Db 881 CGTGTCTGAGAAATCTAGAGCATCTCTCTTACCGCCCTCAAGTACTATCTTCAAGACC 940
Qy 662 AAAAGCCGTTGTGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 721
Db 941 CACGACCGCTCTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1000
Qy 722 TCGAGAGAGCGGCTGTCTCTGAGAGACGACAGCTTCTATGATGAGAAATGCTCTCT 781
Db 1001 TCTCGAGAGCGGCTGTCTCTGAGAGACGAGCGGCGGCTCTATGATGAGAAATGCTCT 1060
Qy 782 GCTTGAAGTATCTATCTATCTGAGAAAG--TTGTGATCCGTGATCTCAAGTTGAGAA 838
Db 1061 GCCCTGAGACTACTGCACTCCGAGAAAGACGTGTGTACCGGACCTGAAAGCTGAGAA 1120
Qy 839 CTAAAGCTGAGAAAGATGAGCCACATTAATAATTAAGATTTTGGATTTTGGAAAGAG 898
Db 1121 CTGATGCTGAGAAAG 1180
Qy 899 ATCAGAGATGAG 958
Db 1181 ATCAGAGATGAG 1240
Qy 959 GTGTTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1018
Db 1241 GTGCTGAGAGACAAAGCATACGCGCGGTGATGATGATGATGATGATGATGATGATGAT 1300
Qy 1019 TATGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1078
Db 1301 TATGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1360
Qy 1079 TTAATATTAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1138
Db 1361 CTGATCTCATGAGAGAGATCCGCTTCCGCGCAACTCGGCTGAGGCCAAGTCCCTG 1420
Qy 1139 CTTTCAAGGCTCTGTATTAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1198
Db 1421 CTCTCCGCGCTGCTCAAGAAAGACCTTACACAGAGGCTCGGAGGCTCTGAGATGCC 1480
Qy 1199 AAAAGAAATTAAG 1258
Db 1481 AAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1540
Qy 1259 AAGCTTGTACCTCTTTTAAACCTCAAGTAAATCTGAGAGAGATGATGATGATGAT 1318
Db 1541 AAGCTGAGCCACCTTTTCAAGGCCAAGTCACTCTGAGAGAGATGATGATGATGAT 1600
Qy 1319 GAGAGATTCACAGCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1654
Db 1601 GAGAGATTCACAGCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1714
Qy 1379 ATGAGCTGATGAG 1438
Db 1655 ATGAGCTGTGAG 1714
Qy 1439 GAGAGAGATTAAGTC 1453
Db 1715 GGCACAGCTGAGGC 1729

RESULT 7

ORGANISM: Mus musculus
US-10-735-461-20

Query Match 48.6%; Score 751.4; DB 19; Length 2626;

Best Local Similarity 71.8%; Pred. No. 2.3e-190;

Matches 1044; Conservative 0; Mismatches 396; Indels 15; Gaps 4;

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QY      8 ATCATGAGCATGTATACCATGTGTGAAGAAGGTGGGTTCAAGAGAGGGAGAAATATATA 67
DB      281 ACCATGAACGAGTGAAGCATTTGTGAAGAGGGCTGGCTGCACAAACGAGGGAAATATNT 340
QY      68 AAAAATGAGGCGCAAGATACTTCTTTTGAAGACAGATGCTCATTCATAGATATATA 127
DB      341 AAAACCTGGCGGCGACGCTACTTCTCTCAAGAAAGATGCACTTTATTTGGCTACAG 400
QY      128 GAGAAACCTCAAGATGTGAT---TTACTTATCCCTCAACACATTTTCACTGGCAAA 184
DB      401 GAACGAGCTCAAGATGTGATGACGAGAGTCCCACTCAACAACTTCTCACTGGCAAA 460
QY      185 TGCCAGTTATGAAAAACAGAACGACCAAGCAACATTTATATATCATGATGTCTCAG 244
DB      461 TGCCAGCTGATGAAGCAGAGGCGCAAGGCCAACACTTTATCATCCGCTGCTGCAG 520
QY      245 TGGACTACTGTTATAGAGAAATTTCACTGATGATCTCCAGAGAAAAGGAAAGATG 304
DB      521 TGGACCAACGATGTAGGCGCACTTCCATGTGAAAACGCTGAGGAGCGGAAAGATG 580
QY      305 AAGAAAGCTATCCAGGCTGTAGCAGACAGCTGAGAGGCAAGAAAGAGAGATGAT 364
DB      581 GGCACCGCATTCAGCTGTGACCGATGACCTCAAGAGGCAAGAAAGACAGATGAC 640
QY      365 TGTAGTCCAACTTCAAAATTTGATATATATAGAGAGAGATGATGCTCTCAACC 424
DB      641 TTCGATCAGGCTCAACCCAGTGAACCTCAGGGGCTGAAGATGAGGTGTCCCTGGCC 700
QY      425 CATC---ATAAAAGAAAGCAATGAATGATTTTGAATTTTGAATTTTGAATTTTGA 481
DB      701 AAGCCAGACACCGTGTGACATGAACGATTTGATGATCTCAAACTACGCGCAAGGAC 760
QY      482 ACTTTGGGAAAGTTATTTGGTGGAGAGAGGCAAGGAAATATCATGCTATGAAAG 541
DB      761 ACTTTGGGAAAGTTATTTGGTGGAGAGAGGCAAGGCGGCTACTATCATGAAAG 820
QY      542 ATTCTGAAGAAAGAGTCAATTTATGCAAGATGAGTGGCAACACTCTTAACCTGAAGC 601
DB      821 ATCTCAAGAAAGAGTCAATGCTGCGCAAGATGAGTGGCCACACGCTTACTGAGAC 880
QY      602 AGAGTATTAAGAAACATGACATCCCTTTTAAACATCTTGAATATTTCTTCCAGAC 661
DB      881 CGTGTCTGCAAGAACTGAGGATCCCTTCTTACGCGCCCTCAAGTACTCATTTCCAGAC 940
QY      662 AAAAGCCGTTGTGTTTGTGATGGAATATGTTAATGGGGGAGGCTGTTTCCATTG 721
DB      941 CACGACCCGCTCTGCTTTGTCAATGAGATGACCAAGGGGAGAGCTCTTCTTCCACTG 1000
QY      722 TCGAGAGAGCGGGGTGTTCTCTGAGACCGCACAGCTTTATGTGTCAGAAATTTGCTCT 781
DB      1001 TCTCGAGAGCGGGGTGTTCTCCGAGGACCGGGCCGCTTTATGATGTCGAGATTTGTCT 1060
QY      782 GCGTTGATATCTACATTCGGAAGAA---TTGTGATCCGATGATTCAGTTGAGAAAT 838
DB      1061 GCGCTGATCTACTTGTGACTCCGAGAAAGACGTGTGTACTCGGAGACTGAAAGCTGGAAC 1120
QY      839 CTAATGCTGGAACAAAGATGGCCACATTAATAATTAAGATTTTGACTTTGCAAGAGGG 898
DB      1121 CTCATGCTGGAACAAAGACGGGCACTCAAGATTAACGACTTCGGGTGTGCAAGAGGGG 1180
QY      899 ATCAAGATGACGACCACTGAAGACATTTCTGTGCACTCCAGAAATATCTGCACAGAG 958
DB      1181 ATCAAGATGATGACCACTGAAGACATTTCTGCGAAGCGCGAGATGACTGCGCCCTGAG 1240
QY      959 GTGTTAAGATTAATGATCTATGCGGAGAGTGAAGTGTGTGGGCTTGAAGGCTTGTGATG 1018

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DB      1241 GTGCTGAGACCAACGACTACGCGCCGTGACATGACGTGTGGGCGCTGGCTGATCAG 1300
QY      1019 TATGAATGATGTGTGGAGGTTACTTTCTTCAACACGAGACCATGAGAACTTTTGA 1078
DB      1301 TATGAGATGATGTGTGGCGGCTGCTTCTTCAACACGAGACCATGAGAGCTTTTGA 1360
QY      1079 TTAATATTAATGAGACATTAATAATTTCTCGAACACTCTTTCAGATGCAAAATCATTTG 1138
DB      1361 CTGATCTCATGAGAGAGATCCGCTTCCGCGCACACTCGGCTTGAAGCCAGTCCCTG 1420
QY      1139 CTTTCAAGGCTCTTATTAAGATTCATAATAAGCCTTTGTGAGAGACAGATGATGCA 1198
DB      1421 CTCTCGGCGCTCTCAAGAGACCTTCAACAGAGCTCTGGTGGGCGCTTGAAGATGCG 1480
QY      1199 AAAGAATTAATGAGACACAGTTTCTTCTGTGAGTAACTGGCAGATGATATGATATA 1258
DB      1481 AAGGATCATGACACACCGGTTCTTTTGCACACATGCTGTGACAGAGTGTATAGAG 1540
QY      1259 AAGCTTGAACCTCTTTTAAACCTCAAGTAACTCTGAGACAGATATAGATTTTGTAT 1318
DB      1541 AAGCTGAGCCCACTTTCAAGCCCAAGTCACTCTGAGACTGACACCGGATTTTCAAT 1600
QY      1319 GAGAAATTTTACGCTCAAGCTATTTTCAATTAACACCACTGAAAAATATGATGATGAT 1378
DB      1601 GAGAGTTTCAAGCTCAAGATGATCAACATCAACGCGCTG-----ATCAAGATGACAC 1654
QY      1379 ATGAGCTGATGACATGAGAGAGGCGCGCATTTCCCTCAATTTTCTACTCTCAAGT 1438
DB      1655 ATGAGTGTGTGAGATGAGAGGAGGCGGACCTTCCCGAGTTCTCTACTACAGCACT 1714
QY      1439 GGACGAGATTAAGTC 1453
DB      1715 GGCACAGCCTGAGGC 1729

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RESULT 9

US-10-895-225A-56
Sequence 56, Application US/10895225A
Publication No. US20050048587A1

GENERAL INFORMATION:

APPLICANT: Rao, Patricia
APPLICANT: Snyder, Jessica
APPLICANT: Bagley, Andria
TITLE OF INVENTION: METHODS FOR IDENTIFYING TOLERANCE
FILE REFERENCE: TLN-025
CURRENT APPLICATION NUMBER: US/10/895,225A
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: 60/488,502
PRIOR FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 161
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 56
LENGTH: 2626
TYPE: DNA

ORGANISM: Homo sapiens
US-10-895-225A-56

Query Match 48.6%; Score 751.4; DB 19; Length 2626;

Best Local Similarity 71.8%; Pred. No. 2.3e-190;

Matches 1044; Conservative 0; Mismatches 396; Indels 15; Gaps 4;

```

QY      8 ATCATGAGCATGTATACCATGTGTGAAGAAGGTGGGTTCAAGAGAGGGAGAAATATATA 67
DB      281 ACCATGAACGAGTGAAGCATTTGTGAAGAGGGCTGGCTGCACAAACGAGGGAAATATNT 340
QY      68 AAAAATGAGGCGCAAGATACTTCTTTTGAAGACAGATGCTCATTCATAGATATATA 127
DB      341 AAAACCTGGCGGCGACGCTACTTCTCTCAAGAAAGATGGAACCTTTATTTGGCTACAG 400
QY      128 GAGAAACCTCAAGATGTGAT---TTACTTATCCCTTCAACAACTTTTCACTGGCAAA 184
DB      401 GAACGCTCAAGATGTGATGACGAGAGTCCCACTCAACAACTTCTCACTGGCAAA 460

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Db      690 GCCAAGCCCAACACCGCGTGAACATGAACGATTGAGTACTGTAAGCTGCGGCAAG 749
Qy      479 GGCACCTTTGGAAAGTTATTTTGTGTCAGAGAGGCAAGGAAATATCATGTGTAG 538
Db      750 GGCACCTTTGGAAAGTTATTTTGTGTCAGAGAGGCAAGGAAATATCATGTGTAG 809
Qy      539 AAGATTCTGAAGAAAGAAAGTCAATTTATGCAAGAGTGAAGTGCACACTCTAACTGAA 598
Db      810 AAGATCTCAAGAAAGAAAGTCAATTTATGCAAGAGTGAAGTGCACACTCTAACTGAA 869
Qy      599 AGCAGATTTAAAGAACTAGACATCCCTTTTAACTCTTGAATATTCCTTCAG 658
Db      870 AACCGGCTCTCAGAACTCCAGGACCCCTTCTCAGACCCCTGAAGTACTTCTCAG 929
Qy      659 ACAAAAGACGTTTGTGTTTGTGATGAGAAATGTTAAGGGGGGAGAGTGTTCAT 718
Db      930 ACCCAGACCGCTCTGCTTTGTGATGAGTACGCCAAGGGGGGAGAGTGTTCAT 989
Qy      719 TTGTCGAGAGAGCGGGTGTCTCTGAGACCGCACAGTTCATGAGTGCAGAAATGTC 778
Db      990 CTGTCCCGGAGAGGTGTGTCTCTGAGACCGGGCCCGCTTCTATGCGCTGAGATGTC 1049
Qy      779 TCTGCTTGGACTATCTAATTCGGAAGA--TTGTACCGGTGATCTCAAGTTGAG 835
Db      1050 TCAGCCCTGACTACTGCACTCGAGAGAAAGCTGTGTACTACCGGAGCTCAAGCTGAG 1109
Qy      836 AATCTAATGCTGAGCAAAAGATGCGCACATTAATAATGAGATTTTGAATTTGCAAAAG 895
Db      1110 AACCTCATCTGAGCAAGAGCGGACATTAAGATACAGACTCGGGCTGTGCAAGAG 1169
Qy      896 GGGATCACAGATGACGCCACATGAGACATTCGTGAGACTCCAGATATCTGAGCA 955
Db      1170 GGGATTAAGAGAGGTGCGCACATGAGACCTTTTGGGACACCTGAGTACTGCGCCC 1229
Qy      956 GAGGTGTTAAGATATATGATGAGCGCAGAGTGAAGTGTGGGCTTACGGGTTGTC 1015
Db      1230 GAGGTGCTGAGAGACATGACGCGCGTGAAGTGAAGTGTGGGCTGAGGCTGTC 1289
Qy      1016 AAGTATGAATGATGTGTGGAGGTTACCTTCTACACAGAGACCATGAGAACTTTT 1075
Db      1290 AAGTATGAATGATGTGTGGAGGTTACCTTCTACACAGAGACCATGAGAACTTTT 1349
Qy      1076 GAATTAATTAATGAGAGACATTAATTTCTGACACACTCTCTTCAAGTGCAGAAATCA 1135
Db      1350 GAGTCATCTCATGAGAGAGATCCGCTTCCCGGACGCTTGTGCGAGGCCAAGTCC 1409
Qy      1136 TTGCTTTCAAGGCTCTTGAATGAAGATCCAAATPAAAGCTTGTGTGAGAGCAAGTAT 1195
Db      1410 TTGCTTTCAAGGCTCTTGAATGAAGATCCCAAGCAGAGGCTTGTGCGGAGCTCCGAGGAC 1469
Qy      1196 GAAAAGAAATTAATGAGACAGTTCCTCTGAGATGAATGCGCAATATTAATGAT 1255
Db      1470 GCAAGAGATCATGAGATGATGCTTCTTTCGCGATGTGTGTGAGAGCACTGATGAG 1529
Qy      1256 AAAAGCTTGTACTCTCTTTTAACTCAAGTAAACATCTGAGACAGATACTAGATTTT 1315
Db      1530 AAGAGCTCAGGCCACTTTCAGAGCCCAAGTCAAGTGCAGAGTGCAGACAGATTTT 1589
Qy      1316 GATGAAGATTTAAGCTCAGACTATTAATTAATTAACCACTGAAATATATGATGAGT 1375
Db      1590 GATGAGAGTTCAGCGCCAGATGATCAATCAACCACTGAGCCAA-----GATGAC 1643
Qy      1376 GGTATGAGATGAGAGCAATGAGAGGCGCGCATTTCCCTCAATTTCTACTGTGA 1435
Db      1644 AAGATGAGATGTGTGAGAGCAAGAGCGCAAGCCCACTTCCCAAGTTCTTACTGAGC 1703
Qy      1436 AGTGAAGAGAAATGATC 1453
Db      1704 AGCGGACGCGCTGAGGC 1721
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RESULT 11

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US-09-955-999-43
; Sequence 43, Application US/09955999
; Publication No. US20030036505A1
; GENERAL INFORMATION:
; APPLICANT: Barash et al.
; TITLE OF INVENTION: Signal Transduction Pathway Component Polynucleotides, Polypeptide
; FILE REFERENCE: PTO86P1
; CURRENT APPLICATION NUMBER: US/09/955,999
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 2978
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (28)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2947)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2973)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-955-999-43
```

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Query Match          46.7%; Score 722.4; DB 10; Length 2978;
Best Local Similarity 70.4%; Pred. No. 1.5e-182;
Matches 1027; Conservative 0; Mismatches 416; Indels 15; Gaps 4;
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Qy      5 GTCATCATGAGCGATGTTATCCATTGTGAAGAAGTTGGCTTCAGAAAGGAGAAATAT 64
Db      485 GGCACCATGAGAGAGTGTGCTATTTGTGAAGAGGTTGGCTGCACAAACGAGGAGATAC 544
Qy      65 ATAAAAATGAGAGCGCAAGATCTTCTTTGAAGACAGATGGCTCATCTTATGATAT 124
Db      545 ATCAAGACTTGGCGGCCACGCTACTTCTCTCTCAAGAAATGATGCACTTCACTTGGCTAC 604
Qy      125 AAAAGAAACCTCAAGATGTGATTTAATTCTTCCCTCAACAACTTTTCAAGTGCA 181
Db      605 AAGAGCGCGCGCAGAGATGTGACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 664
Qy      182 AATGCGATTAATGAAGAAACAGACCAAGCAACCAACATTTATATCAAGTGTCTC 241
Db      665 CAGTCCAGCTGATGAAGAGCGAGCGGCCGCCCAACACCTTCATCATCGCTGCTG 724
Qy      242 CAGTGAATCACTGTATGAGAGAACTTTCATGTGATGATCTCCAGAGAAAGGAGAA 301
Db      725 CAGTGAATCACTGTATGAGAGAACTTTCATGTGATGATCTCCAGAGAAAGGAGAA 784
Qy      302 TGAAGAGAACTTATCAGGCTGTAGACAGACTGACAGAGGCAAGAGAGAGAGAAATG 361
Db      785 TGAAGAGAACTTATCAGGCTGTAGACAGACTGACAGAGGCAAGAGAGAGAGAAATG 844
Qy      362 AATGTGATCAACTTCAAAATGATTAATATGAGAGAGAGAGAGAGAGAGAGAGAGAG 421
Db      845 GACTTCCGCTCGGCTCAGCCAGTGAACATCAAGAGGCTGAAGAGATGAGAGTGTCCCTG 904
Qy      422 ACCCAT---ATAAAGAAAGCAATGATGATTTTGAATTTGAATCTAGATTA 478
Db      905 GCAAGCCCAAGCAGCGGTGACATGAACGATTTGATGATCTAAGCTGTGAGCAAG 964
Qy      479 GGCATTTTGGAAAGTTATTTTGTGTCAGAGAGGCAAGTGAAGAAATATCATGTGTAG 538
Db      965 GGCATTTTGGAAAGTTATTTTGTGTCAGAGAGGCAAGTGAAGAAATATCATGTGTAG 1024
Qy      539 AAGATTCTGAAGAAAGAAAGTCAATTTATGCAAGAGTGAAGTGCACACTCTAACTGAA 598
Db      1025 AAGATCTCAAGAAAGAAAGTCAATTTATGCAAGAGTGAAGTGCACACTCTAACTGAA 1084
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QY 599 AGGAGATATTAAAGAACTAGACATCCCTTTTAACTCTTGAATAATTCCTCCAG 658
DB 1085 AACCGGCTCTGAGAACTCAGGCAACCCCTTCTCAACAGCCCTGAAGTACTCTTCCAG 1144
QY 659 ACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTATGGGGGCGAGCTGTTTTCCAT 718
DB 1145 ACCCAAGACCGCTCTGCTTGTGTCATGAGTACGCCAAGGGGGGCGAGCTTCTCCAC 1204
QY 719 TTGTGAGAGAGCGGGGTGTTCTCTGAGAGACCGCAACGTTTCTATGCTGAGAAATGTC 778
DB 1205 CTGTCCCGGAGCGGTGTTCTCCGAGAGACCGGGCCCGCTTCTATGGCGCTGAGATTGTG 1264
QY 779 TCTGCTTGAATCTATCTACATTCGGAAAAGAAA---TTGTGATCCGTATCTCAAGTTGAG 835
DB 1265 TCGACCTGAGACCTGACCTGAGAGAAAGCGTGTGTGACCGGAGCCTCAAGCTGAGAG 1324
QY 836 AATCTAATGCTGAGCAAAAGATGCGCACATATAAATTACAGATTGTTGACTTTGCAAAAG 895
DB 1325 AACTCATGCTGAGCAAGAGACGGGACATTAAATCAAGACTTCGGGCTGTGCAAGAG 1384
QY 896 GGGATCAAGAGTCAAGACCATGAGACATCTGTGCACTCCAGAAATATCTGGACCA 955
DB 1385 GGGATCAAGAGCGGTGCAACATGAGAGACCTTTTGGGCGCACACTGATGACTGGCCCC 1444
QY 956 GAGGTGTGAAGATATATGATCTATGCGCGAGAGTACGTGTGGGCGCTAGGGGTTGTC 1015
DB 1445 GAGGTGTGAGAGCAATGATCTACGGCGGAGTACGTGTGGGCGCTAGGGGCTGAGTGC 1504
QY 1016 ATGTATGAATATGATGTGTGAGAGTTTACTTTTCAACACAGGACCATGAGAACTTTT 1075
DB 1505 ATGTATGAAGATATGTGTGCGGTGCGCTGCTTCTACACAGAGCATGAGAACTTTT 1564
QY 1076 GAATTAATATTAATGAGACATTAATTTCTCGAACACTCTTCTCAATGCAAAATCA 1135
DB 1565 GAGCTCATCTCATGAGAGAGATCCGCTTCCGCGGACGCTTGTCGCCGAGGCCAAGTCC 1624
QY 1136 TTGCTTTCAAGGCTCTTGAATAAAGATCCAAATTAAGCTTGTGTGAGAGACAGATGAT 1195
DB 1625 TTGCTTTCAAGGCTCTGCAAGAAAGACCCCAAGCAGGCTTGTGGGGGCTCCGAGAC 1684
QY 1196 GCAAAAGAAATTAATGAGACACAGTTTCTCTGAGTAAACTGGCAAGATGATATGAT 1255
DB 1685 GCCAAGAGATCTATGACGATCGCTTCTTGGCGGATGCTGTGCGACGACGCTGACGAG 1744
QY 1256 AAAAAGCTGTACTCTCTTTTAACTCAAGTAAATCTGAGACAGATTAAGATATTTT 1315
DB 1745 AAGAACTGACCCCACTTCAAGCCCAAGTCAAGTCAAGTCAAGTCAAGTATTTT 1804
QY 1316 GATGAAGATTTTACAGTCTCAAGTATTAACAATCAACACCTGAAAATATGATGAGAT 1375
DB 1805 GATGAAGAGTTTCAAGGCGCCAGATGATCAATCAACACCTGACCA-----GATGAC 1858
QY 1376 GGTATGACTGATGAGCAATGAGAGCGCGGATTTCCCTCAATTTTCTTACTGCTGCA 1435
DB 1859 AGCATGAGTGTGTGAGACGAGCGAGCGAGGCCCACTTCCCAAGTCTTCTTCTGAGCC 1918
QY 1436 AGTGAAGAGAAATTAAGTC 1453
DB 1919 AGCGGACAGGCGCTGAGGC 1936
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```
RESULT 12
US-10-072-036-138
; Sequence 138, Application US/10072036
; Publication No. US20030082564A1
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP
; APPLICANT: Sara BURON
; APPLICANT: Soren TULLIN
; APPLICANT: Kasper ALMHOLT
; APPLICANT: Kurt SCUDDER
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An I
```

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; TITLE OF INVENTION: On A Cellular Response
; FILE REFERENCE: 3759-0120P
; CURRENT APPLICATION NUMBER: US/10/072,036
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/417,197
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 138
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EGFP-PXB fusion
; NAME/KEY: CDS
; LOCATION: (1)..(2181)
US-10-072-036-138

Query Match 46.6%; Score 721.2; DB 14; Length 2184;
Best Local Similarity 70.7%; Pred. No. 2,6e-182;
Matches 1021; Conservative 0; Mismatches 408; Indels 15; Gaps 4;

QY 3 GAGTCATCATGAGCCGATGTTACATTTGTAAGAAAGTTGGGTTGAGAGAGGAGAAAT 62
DB 734 GAGGCACTGAGACGACGCTGCTATTGTGAAGAGGTTGGCTGCAAAACAGAGGAGAT 793
QY 63 ATATATAAACTGAGAGCCAGATATCTTCTTTGAAGACAGATGCTCATTAAGAT 122
DB 794 ACATCAAGACCTGAGCGGACGCTACTTCTCTCAAGATATGAGCACTTCAATGGCT 853
QY 123 ATTAAGAAAGCTCAAGATGTGATTTACCTTA---TCCCTCAACAACTTTTCAAGT 179
DB 854 ACAAGAGAGGCGCGCAGATGTGACCAACGTGAGGCTCCCTCAACAACTTCTGTGG 913
QY 180 CAAATAGCCAGTTAATGAAGAAAGAAAGCAACCAAGCCAAACACATTTATATCAGATGTC 239
DB 914 CGAGTGCAGCTGATGAAGAGAGAGCGGCCCGGCCCAACACTTCAATCATTCGCTGCC 973
QY 240 TCCAGTGAATCTGTTATGAGAGAACTTCTATGATGATATCTCCAGAGAAAGGAAAG 299
DB 974 TGAGTGTGAGCACTGTCATGAGACGCACTTCATGATGAGACTCTGAGAGCGGAGAG 1033
QY 300 AATGACAGAACTATCCAGGCTGTAGCAAGACAGACTGACAGGCGCAAGAGAGAGAA 359
DB 1034 AGTGAACAAACCGCACAACGACTGTGCTGAGAGGCTCAAGAAAGCAGAGAGAGAGAG 1093
QY 360 TGAATGTATGTCCAACTGACAAATGATATATATGAGAGAGAGAGATGATGCTCTTA 419
DB 1094 TGAGTCTCGGTGCGGCTACCAAGTACCACTCAGGGGCTGAAGAGATGAGGTGCC 1153
QY 420 CAACCCATC---ATATAAGAAAGACAAATGATGATTTTGAATTTTGAATCTAAGAT 476
DB 1154 TGAGCCAAAGCCAAAGACCGCGTGAACATGAAGAGATTTGATGATGATGATGAGT 1213
QY 477 AAGGCACTTTTGGGAAAGTATTTTGTGAGAGAGAGCAAGTGAAGAAATACTATGCTA 536
DB 1214 AAGGCACTTTTGGGCAAGTATCTGTGTGAAGAGAGAGCAAGGCGCTCTACTAGCCA 1273
QY 537 TGAAGATCTGAAGAAAGAGTCAATATGCAAAAGATGAAGTGGCAGACACTTAAGT 596
DB 1274 TGAAGATCTCAAGAGAGAGATCTGTGCGCAAGAGAGAGTGGCCCAACACTACCG 1333
QY 597 AAAGCAGATATTAAGAACTAGACATCCCTTTTAACTCTTGAATAATTCCTTCC 656
DB 1334 AGAACCGGTCTGAGAGAACTCAGGCAACCTTCTCTCAAGCCCTGAAAGTACTCTTCC 1393
QY 657 AGACAAAAGACCGTTGTGTTTGTGATGAGATATGTTAATGGGGCGAGCTGTTTCC 716
DB 1394 AGACCCAGACCGCTGTGCTTGTGATGAGATGAGCAAGGGGCGAGCTGTTTCC 1453
QY 717 ATTTGCGAGAGAGCGGTGTTCTCTGAGAGACCGACAGTTTCTATGCTGAGAAATGG 776
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Db 1454 ACCGTCCGGGAAAGCTGTCTTCGAGACCGGCCCGCTTCTATAGCGCTGAGATTG 1513
 QY 777 TCTCTGCTTGGACATCTACATTCGGAAAG--TTGTATACCGTATCTCAAGTTGG 833
 Db 1514 TGTCAAGCTTGGATCTCTGCACTCGAAGAGACCTGTGTACCGGACCTCAAGCTGG 1573
 QY 834 AGAATCTAATGCTGACAAAGATGCGCACATATAAAATTAACAATTTTGGACTTTGCAAG 893
 Db 1574 ACAAACCTATGCTGACAAAGACCGGCAATTAAGATCAACAAGCTTCGGGCTGTGCAAG 1633
 QY 894 AAGGATTCACATGACGCCACCATTAAGACATTTCTGTGGCACTCCAGATATCTGGCAC 953
 Db 1634 AAGGATTCACAGACCGGTGCGACCATTAAGACCTTTTGGCGCACTCTGATCTGGCCC 1693
 QY 954 CAGAGGTGTAAGATTAATGACTATAGCGCGACAGTATAGTGTGGGCGCTAGGGGTTG 1013
 Db 1694 CCGAGGTGCTGAGAGCAATGACTACGCGCGTGCAGTGAATGTGTGGGGCTGGGGCTGG 1753
 QY 1014 TCATGTATGAAAATGATGTGTGGAGGTACCTTTTACAACGACGACATGAGAACTTT 1073
 Db 1754 TCATGTACGAGATGATGTGCGGTGCGCTGCGCTTCTACAAACGACGACATGAGAACTTT 1813
 QY 1074 TTGAATTAATTAATGAGAGACATTAATTTCTTGAAACACTCTTTCAAGATGCAAAAT 1133
 Db 1814 TTGAAGCTCATCTCATGAGAGAGATCCGCTTCCCGGACGCTTGTGTCGAGGCCAAGT 1873
 QY 1134 CATGCTTTCAGGGCTCTTGATTAAGATTCAAAATTAAGCGCTTGGTGGAGACCGAGATG 1193
 Db 1874 CTTGCTTTCAGGGCTGCTCAAGAGACCCCAAGAGAGGCTTGGCGGGGCTCCGAGG 1933
 QY 1194 ATGCAAAAGAAATTAAGACACAGTTTCTCTGAGTAAACTGGCAAGATGATATATG 1253
 Db 1934 ACGCCAGAGATCATGAGACATCGCTTCTTGGCGGTATCGTGTGGACGACGATAG 1993
 QY 1254 ATAAAAAGTTTGTACTCTCTTTTAACTCAAGTAACTATGAGACAGTACTAATAT 1313
 Db 1994 AAGAAAGTCAAGCCCACTTCAAGCCCAAGTCAAGTGAAGTCAACACAGATAT 2053
 QY 1314 TTGATGAATTAATTAAGCTCAGACTATTAACAATACACCACTGAAATATGATGAG 1373
 Db 2054 TTGATGAGAGATTCACGCGCCAGATATCAACATCAACACCTGACCA-----GATG 2107
 QY 1374 ATGATGAGACTGATGACAAATGAGAGCGCGCGCATTTCCCTCAATTTTCTACTCTG 1433
 Db 2108 ACAGCATGAGATGTGTGACAGGACGAGCGGCGCCACTTCCCGCACTTCTCTACTCG 2167
 QY 1434 CAAG 1437
 Db 2168 CCAAG 2171

RESULT 13
 US-09-970-000-3
 Sequence 3, Application US/0970000
 Patent No. US20020127214A1
 GENERAL INFORMATION:
 APPLICANT: Hemmings, Brian Arthur
 TITLE OF INVENTION: Rac-Protein Kinase as Therapeutic Agent
 Or In Diagnostics
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. US20020127214A1
 STREET: 564 Morris Avenue
 CITY: Summit
 STATE: NJ
 COUNTRY: USA
 ZIP: 07901-1027
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/970,000
 FILING DATE: 03-Oct-2001
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/068,702
 FILING DATE: 13-May-1998
 APPLICATION NUMBER: PCT/EP96/04810
 FILING DATE: 11-May-1996
 APPLICATION NUMBER: GB 9523379.7
 FILING DATE: 16-May-1995
 APPLICATION NUMBER: US20020127214A1-1995
 FILING DATE: 15-Dec-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Furman, Diane E.
 REGISTRATION NUMBER: 31,104
 REFERENCE/DOCKET NUMBER: 4-20635/A/PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 522-6924
 TELEFAX: (908) 522-6955
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2610 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: Human RAC alpha
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 199..1641
 NAME/KEY: mat_peptide
 LOCATION: 199..1641
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-970-000-3

Query Match 46.5%; Score 719.2; DB 9; Length 2610;
 Best Local Similarity 70.3%; Pred. No. 1e-181;
 Matches 1025; Conservative 0; Mismatches 418; Indels 15; Gaps 4;

QY 5 GTCAATCAGAGGAGATTACCATTTGAAAGAGGTTGGTTCAGAGAGGAGAAATAT 64
 Db 193 GGCACATGAGCGACGCTGATTTGTGAAGAGGTTGGCTGCAAAAGAGGAGATG 252
 QY 65 ATAAAACTGAGGCCAAGATCTCTTTTGAAGACAGATGCTCATTTAGATAT 124
 Db 253 ATCAAGACTGCGCGCCAGCTACTTCTCTCAAGATGATGCACTTATGGCTAC 312
 QY 125 AAAAGAACTCAAGATGTGATTTACCTTA--TCCCTCAACAATTTCAATGGCA 181
 Db 313 AAGAGCGCGCCAGATGTGACCAAGTGTAGGCTCCCTTCMAAATCTCTGTGGCG 372
 QY 182 AAATCGCATTAATGAAACAGAACGACCAAGCCAAACACATTTATATAGATGTCTC 241
 Db 373 CAGTCCAGCTATTAAGAGAGAGCGGCGCGCCCAACACTTATATATCTGCTGCTG 432
 QY 242 CAGTGAATCTGTTATAGAGAAATTTATGATGATCTCAAGAGAAAGAGAGAA 301
 Db 433 CAGTGAACACTGTATGAGAGCACTTCAATGTGAGACTCTGAGAGAGGAGAGAG 492
 QY 302 TGGACAAAGCTATTCAGAGCTGTAGACAGACTGCAAGAGGCAAGAAAGAGAGATG 361
 Db 493 TGGACAAAGCTATTCAGAGCTGTAGACAGACTGCAAGAGGCAAGAGAGAGAGATG 552
 QY 362 AATTGATGCCAATCTCAATTTGATATATATGAGAGAGAGAGAGATGATGCTTCA 421
 Db 553 GACTTCGGGTGCGGCTCAAGAGTGAATCTCAGAGGCTGAAGAGATGAGTGTCTCG 612
 QY 422 ACCCATC--ATAAAGAAAGACATGATGATTTTGAATATTTGAATTAATTAAGTAA 478

Db 613 GCCAAGCCCAAGACCGCGTACCATGAGAGTTTAACTGAACTGCTGGGCAAG 672
Qy 479 GGCACCTTTGGGAAAGTATTTTGGTTCGAGAGAGCAAGTGGAAATATCTATGCTATG 538
Db 673 GGCACCTTTGGGCAAGGATGATCTGCTGTAAGAGAGAGCCACAGGCCCTACTAGCCCATG 732
Qy 539 AAGATTCTGAAGAAGAGTATTAATTGCAAGAAGTAAAGTGGACACACTTAATCGAA 598
Db 733 AAGATCTCTCAAGAGAGAGTATGTCGCCAAGAGAGAGTGGTCCCAACAATCTACACGAG 792
Qy 599 AGCAGAGTATTAAGAACACTAGACATCCCTTTTAAATCATCTTGAATATTCCTTCAG 658
Db 793 AACCGGCTCTGAGAGAGTCCAGGACCCCTTCTCAGACGCCCTGAAGTACTCTTCCTCAG 852
Qy 659 ACAAAAGACCGTTTGTGTGTTTGGTATGAAATATGTAATGGGGGCGAGCTTTTCAT 718
Db 853 ACCCACACCGCCCTGCTTGTGTCATGAGTACGCCAACGGGGGCGAGCTGTTCTTCAC 912
Qy 719 TTGTCGAGAGAGGGGTTCTCTGAGAGACCGCACAGTTTCTATGGTGGAGAAATGTC 778
Db 913 CTGTCCCGGAGACGTGTGTTCTCGAGAGACCGGCGCTTCTATGGCGCTGAGATTGTG 972
Qy 779 TCTGCTTGGACTATCTACATTCGGAAGAAG---TTGTATACCGTGAATCTCAATTGGAG 835
Db 973 TCAGCCCTGAGACTACCTGCACTCGAGAGAGAGACGTGTGTATCCGGGACCTCAAGCTGGAG 1032
Qy 836 AATCTAATGCTGCAAAAGATGCGCACATTAATAATTAAGATTTTGGACTTTGCAAGAA 895
Db 1033 AACCTCATGCTGGCAAGAGACGGGACATTAAGATCAACAATTCGGGGCTGTGCAAGAG 1092
Qy 896 GGGATCACAATGACGACCAATGAGAACATTCGTGGCACTCCAGAAATTTGGGACCA 955
Db 1093 GGGATCAAGAGCGGTGCAACATGAGAACCTTTTGGCGACACTGTGATCTGGGCCCC 1152
Qy 956 GAGGTGTTAAGATTAATGACTATGCGCAGAGTAACTGCTGGGCGCTTGAAGGGTGTGTC 1015
Db 1153 GAGGTGTCGAGAGCAATGACTAGCGCGTGGAGTGAATGCTGGGGGCTGGCGTGTGTC 1212
Qy 1016 ATGTATGAATATGATGTGTGGAGGTTACTTTTCTACACAACAAGACATGAGAAATCTTTT 1075
Db 1213 ATGTACAGATGATGTGTGGTGGTGGCTGCTCTTCTTACAAACAGAGCAATGAGAACTTTT 1272
Qy 1076 GAATTAATATTAATGAGACATTAATTTCTCGAACACTCTCTTCAATGAGTGAATAATCA 1135
Db 1273 GAGCTATCTCTCAATGAGAGATTCGGTCCCGGACGCTTGGTCCGAGGCGCAAGTCC 1332
Qy 1136 TTGCTTTCAAGGCTCTTGAATAAGATCCAAATTAAGCGCTTGGTGGAGAGACAGATGAT 1195
Db 1333 TTGCTTTCAAGGCTCTCAAGAAAGACCCCAAGAGAGGCTTGGCGGGGCTCCGAGGAC 1392
Qy 1196 GCAAAAGAAATTAAGACACAGTTTCTTCTGAGATTAATCTGGCAAGATGATATGAT 1255
Db 1393 GCCAAGAGATCATGACATCGCTTCTTGGCGGTATGCTGTGGACAGCATGTATAGAG 1452
Qy 1256 AAAAGCTTTACTCTCTTTTAAACCTCAAGTAAATCTGAGACAGTACTATATATTTT 1315
Db 1453 AAGAAAGTCAAGCCACCTTCAAGCCCAAGTCAAGTGGAGACTGACACAGATATTTT 1512
Qy 1316 GATGAAGATTTTCAAGCTCAGACTATTAATTAACACCACTGAAAAATATGATGAGAT 1375
Db 1513 GATGAAGATTTCAAGCGCCCAAGATGATCAATCAACCACTGACCA-----GATGAC 1566
Qy 1376 GGTATGAGCTGCAATGAGCAATGAGAGCGGCGCATTTTCCCTCAATTTTCTTACTGCA 1435
Db 1567 AGCATGAGATGTGTGAGACAGAGCGAGCGACCTTCCCGAGTTCTCTACTGCGGC 1526
Qy 1436 AGTGAAGAGAAATTAATGTC 1453
Db 1627 AGCAGCAGGCGCTGAGGC 1644

RESULT 14

US-10-388-263-329
; Sequence 329, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowert, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freiler, Susan M.
; APPLICANT: Sasnor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Onashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 329
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199) ... (1641)
US-10-388-263-329

Query Match 46.5%; Score 719.2; DB 17; Length 2610;
Best Local Similarity 70.3%; Pred. No. 1e-181;
Matches 1025; Conservative 0; Mismatches 418; Indels 15; Gaps 4;

Qy 5 GTCATATGAGCGATGTTACATTTGGAAGAAGTGGGTTGCAAGAAGGAGAGATAT 64
Db 193 GGCACATGAGCAGCAGCTGCTATTTGAAAGAGGTTGGCTGCAAAAGAGGAGTAC 252
Qy 65 ATAAAAAATGAGGCGCAAGATATCTTCTTTGGAAGACAGATGGCTCATTTAGATAT 124
Db 253 ATCAAGACCTGGGCGGCGCAGCTACTTCTCTCAAGAAATGATGGACCTTCAATGGCTAC 312
Qy 125 AAGAGAAACCTCAATATGATGTTAATCTTA---TCCCTCAACAATTTTATAGTGGCA 181
Db 313 AAGAGACCGCGGAGATGTGACCAACGTAGAGCTCCCTCAACAATTTCTGTGGCG 372
Qy 182 AATGCGAGTTAATGAAAAAGAAAGCAAGCAACCAATTTAATCAATTTAATCAGATGCTC 241
Db 373 CAGTGCAGCTATGAAAGACGAGCGGCCGCCCAACACCTTCAATCCGCTGCTG 432
Qy 242 CAGTGAATATGTTAATGAGAAATTTCAATGATATCTTCAGAGGAAAGGAGAA 301
Db 433 CAGTGAACCACTGTATGAGAGCAAGCACTTCAATGTGAGATCTTGAAGGCGGAGAG 492
Qy 302 TGAAGCAAGCTATCAAGGCTGTAGACAGACTCAGAGGCAAGAGAGAGAGAAATG 361
Db 493 TGAAGCAAGCAATCAAGACTGTGCTGACGCGCTCAAGAAAGAGAGAGAGAGATG 552
Qy 362 AATTGATGCAACTTCACAAAATGATATATATATGAGAGAGAGATGATGCTCTACA 421
Db 553 GATTTCCGCTGGGCTCAACCACTGCACTCAAGGCGTGAAGATGAGAGTGTCTCG 612
Qy 422 ACCCATC---ATTAAGAAAGCAATGAATGATTTTGAATTTGAATCTAGGTAA 478
Db 613 GCCAAGCCCAAGAGACCGCGTGAACATGAGAGAGTTTGAATGAGTGTGGCAAG 672
Qy 479 GGCACCTTTGGGAAAGTATTTTGGTTCGAGAGAGGCAAGTGGAAATATCTATGCTATG 538
Db 673 GGCACCTTTGGGCAAGGTGATCTGTGTAAGAGAGAGGCAAGGCGCTTACTACGCAATG 732
Qy 539 AAGATCTGAAGAAAGATGATTAATTGCAAGATGAGTGGACACACTTAATGAA 598

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Db      733 AAGATCCTCAAGAGAGAGTCAATGTCGCCAAGAGAGAGTGGCCACACACTACCGAG 792
Qy      599 AGCAGAGTATTAAGAACAAGTACATCCCTTTTAACTCTTGAATATTTCTTCAG 658
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RESULT 15
US-10-641-643-1206

; Sequence 1206, Application US/10641643
; Publication No. US20040077003A1

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; Susan G. Stuart

; Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL

; GENE EXPRESSION

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; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 845-4166
; TELEFAX: (650) 845-0555
; INFORMATION FOR SEQ ID NO: 1206:
; LENGTH: 2610 base pairs
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; STRANDEDNESS: single
; TOPOLOGY: linear
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; LIBRARY: GENBANK
; CLONE: g190827
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TITLE Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1440)
AUTHORS Clark, A.G., Glanowski, S., Nielsen, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeleo, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Substitution
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity 93.9%; Pred. No. 0;
Matches 1352; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
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DEFINITION genomic survey sequence.
ACCESSION AY399353
VERSION AY399353.1 GI:39755342
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Clark, A.G., Glanowski, S., Nielsen, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeleo, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302
REFERENCE 2 (bases 1 to 1394)
AUTHORS Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.O.,
Adams,M.D. and Cargill,M.
TITLE Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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DEFINITION genomic survey sequence.
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VERSION AY399352.1 GI:39755341
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
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AUTHORS Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.O.,
Adams,M.D. and Cargill,M.
TITLE Infering nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1440)
AUTHORS Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,

Peritera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
Source location/Qualifiers

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QY 251 ACTGTTATAGAGAAACATTTCTATGATATCTCCAGAGAAAGGAGAAATGACAGAA 310
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QY 311 GCTATCCAGGCTGTAGACAGACTGACAGAGGCAAGAAAGAGAGATGATTTGAT 370
DB 301 GCTATCCAGGCTGTAGACAGACTGACAGAGGCAAGAAAGAGAGATGATTTGAT 360
QY 371 CCAACTTCACAAATGTGATATATAGAGAGAAAGATGATGCTCTCAACCCATCAT 430
DB 361 CCAACTTCACAAATGTGATATATAGAGAGAAAGATGATGCTCTCAACCCATCAT 420
QY 431 AAAAGAAAGCATGATGATTTTGAATTTGAACTACTAGATAAGCACTTTTGGG 490
DB 421 AAAAGAAAGCATGATGATTTTGAATTTGAACTACTAGATAAGCACTTTTGGG 480
QY 491 AAAGTATATTTGGTTCAGAGAGAGCAAGTGAATAATCTATGTAAGATTTGTAAG 550
DB 481 AAAGTATATTTGGTTCAGAGAGAGCAAGTGAATAATCTATGTAAGATTTGTAAG 540
QY 551 AAAAGAGTCATTTATTCGAAAGATGAAAGTGCACACCTTAACTGAAGCAGATATTA 610
DB 541 AAAAGAGTCATTTATTCGAAAGATGAAAGTGCACACCTTAACTGAAGCAGATATTA 600
QY 611 AAGAACCTAGACATCCCTTTTAACTCTTGAATAATCTCTTCAGACAAAAGCCGT 670
DB 601 AAGAACCTAGACATCCCTTTTAACTCTTGAATAATCTCTTCAGACAAAAGCCGT 660
QY 671 TTGTGTTTGTGATGATAATGTTAATGGGGCGAGCTGTTTTCATTTGCGAGAG 730
DB 661 TTGTGTTTGTGATGATAATGTTAATGGGGCGAGCTGTTTTCATTTGCGAGAG 720
QY 731 CGGGTGTCTCTGAGAGCGGACACGTTTCTATGATGAGAAATGTCTCTGCTTGAC 790
DB 721 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 780
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QY 791 TATCTACATTCGGAAGATGTGTACCGTGATCTCAAGTTGAGAGATCTAATGCTGAGC 850
DB 781 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 840
QY 851 AAAGATGGCCACATTAATAATTAAGATTTTGAATTTGCAAAAGAGGATCAAGATGCA 910
DB 841 AAAGATGGCCACATTAATAATTAAGATTTTGAATTTGCAAAAGAGGATCAAGATGCA 900
QY 911 GCCACATTAAGACATTTCTGTGGCACTCCAGATATCTGACACAGAGGTGTAAGAGT 970
DB 901 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 960
QY 971 AATGACTATGGCCGACAGTACAGTGTGGGGCTAGGGGTTGTATGTAAGATGATG 1030
DB 961 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1020
QY 1031 TGTGAGAGTTACCTTTCTACAAACGACGACATGAGAAACTTTTGAATTAATTAATG 1090
DB 1021 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1080
QY 1091 GAAGACATTAATTTCTCTGAAACACTCTCTTTCAGATGCAAAATCATTTCTTCAAGGCTC 1150
DB 1081 GAAGACATTAATTTCTCTGAAACACTCTCTTTCAGATGCAAAATCATTTCTTCAAGGCTC 1140
QY 1151 TTGATTAAGATCCAAATTAAGCGCTTGTGAGAGACAGATGATCAAAAGAAATTAATG 1210
DB 1141 TTGATTAAGATCCAAATTAAGCGCTTGTGAGAGACAGATGATCAAAAGAAATTAATG 1200
QY 1211 AGACACAGTTCTCTCTGAGATTAACCTGCAAGATGATATGATTAAGCTTGTACT 1270
DB 1201 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1260
QY 1271 CCTTTAAACCTCAAGTAACTCTGACAGACATGATATTTGATGAAGATTTAA 1330
DB 1261 CCTTTAAACCTCAAGTAACTCTGACAGACATGATATTTGATGAAGATTTAA 1320
QY 1331 GCTCAGCATTAACATTAACACCTGAGAAATATGAGAGATGATGATGATGATG 1390
DB 1321 GCTCAGCATTAACATTAACACCTGAGAAATATGAGAGATGATGATGATGATGATG 1380
QY 1391 GACATGAGAGGCGGCGGATTTCCCTCAATTTTCTTCTGCAAGTGCAGAGATTA 1450
DB 1381 GACATGAGAGGCGGCGGATTTCCCTCAATTTTCTTCTGCAAGTGCAGAGATTA 1440
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RESULT 5
BUS20318 967 bp mRNA linear EST 12-SEP-2002
LOCUS AGENCOURT 10157385 NIH_MGC_134 Mus musculus cDNA clone
DEFINITION IMAGE:6518260 5', mRNA sequence.
ACCESSION BUS20318
VERSION BUS20318.1 GI:22827844
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1409 row: 1 column: 05
High quality sequence start: 16
High quality sequence stop: 729.

Oy	263	GAACATTTCATGTGATATCTCACAAGGAAAGGAAAGATGGAACAAGAGCTATCCAGGCT	322
Db	61	AGAACATTTCATGTATGATATCACCAAGGAAAGAAAGTGGACGGAACTATCCAGCC	120
Oy	353	GTAGCAGACAGACTGCAGAGGCGAAGAGAGAGATGTAATTGTAGTCCACTTCACAA	382
Db	121	GTAGCCGACCGATTCGCAGAGCGAAGAGGAGAGAGATGAATTGTATGCCAACCTCACAG	180
Oy	383	ATTGATAATTATGGAGAGAGAGATGGATGCTCTTACCAACCCTATCTAAAGAAAGACA	442
Db	181	ATTGTAATATATAGGAGAAAGAAAGATGGATGGTGTCTACAAACCCTATCTAAAGAAAGACG	240
Oy	443	ATGAATGATTTTGACTAATTGTAACCTACATAGGTTAAAGCACTTTGGGAAAGTTAATTGG	502
Db	241	ATGAATGATTTTGACTAATTGTAACCTACTAGTTAAAGCACTTTGGGAAAGTTAATTGG	300
Oy	503	GTTCCAGAGAAAGCGAAGTGGAATAACTATGCTATGATGAAGATTCGAAGAAAGAAAGTCAAT	562
Db	301	GTTCCAGAGAAAGCGAAGTGGAATAACTATGCTATGATGAAGATTCGTAAGAAAGAAAGTCAAT	360
Oy	563	ATTGCAAAAGATGAAGTGCGACACACTCTTAAGTAAAGCAGATTTAAAGAACCTAGA	622
Db	361	ATTGCAAAAGATGAAGTGCGACACACTCTTACTGAAAGCAGATCTAAAGAACACAGA	420
Oy	623	CATCCCTTTTAAACATCCTGTGAATATTCCTCCGACAGAAAGACCGTTTGCTTTGG	682
Db	421	CATCCATTTTAAACATCCTGTGAATATTCCTCCGACAGAAAGACCGTTTGCTTTGG	480
Oy	683	ATGTAATATGTTAATAGGGGGCAGGCTGTTTCCATTTGTCGAGAGAGCGGCTGTTCT	742
Db	481	ATGTAATATGTTAATAGGGGGAGAGCTGTTTCCATTTGTCGAGAGAGCGAGTGTCT	540
Oy	743	GAGGACCGCACACGTTTCTATGTGTGAGAAATTGCTCTGCTTGGACTATCTACATTC	802
Db	541	GAGGACCGCACACGTTTCTATGTGTGAGAAATTGCTCTGCTTGGACTATCTACATTC	600
Oy	803	GGAAGAGATTGTGTACCGTGATCTCAAGTTGAGAGATCTAATGCTGGACAAAGATGGCCAC	862
Db	601	GGAAGAGATTGTGTACCGTGATCTCAAGTTGAGAGATTGATCTAGATAGAGTGGCAAT	660
Oy	863	ATTAATAATTACAGATTTTGACTTTGCAAGAAAGAGGATCACAGATGCAGCCACATGAG	922
Db	661	ATTAATAATTACAGATTTTGGGCTTTGCAAGAAAGAGGATCACAGATGCAGCTACATGAG	720
Oy	923	ACATTCTGTGCACTTCAGAGATATCTGCGACCAAGAGTTTAAAGATATGACTATGGC	982
Db	721	ACATTCTGTGCACTTCAGAGATATCTGCGACCAAGAGTTTAAAGATATGACTATGGC	780
Oy	983	CGAGCAGTAGACTGGTGGGGCCTTAAGGGGTGTCAATGATG	1022
Db	781	CGAGCCGTGACTGGTGGGGCTTAAAGTGTGTCAATGATG	820

RESULT 7	CNS27185	798 bp	mRNA	linear	EST 29-APR-2004
LOCUS	CNS27185				
DEFINITION	UI-H-HB0-epgc-c-10-0-UI-r1 NIH_BMAP_HB0 Mus musculus cDNA clone IMAGE:30653145 5', mRNA sequence.				
ACCESSION	CNS27185				
VERSION	CNS27185.1	GI:4685341			
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 798)				
AUTHORS	NIH-MGC http://mgc.ncl.nih.gov/ .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. James Lin University of Iowa				

CDNA library preparation: Dr. M. Bento Soares, University of Iowa
CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: PYX-5
Location/Qualifiers
1
798

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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30653145"
/tissue_type="whole eye"
/dev_stage="embryo 12.5,13,5,14,5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_11b="NH_BMAP_H80"
/notes="Organ: Eye; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according Bonaldo, Lemmon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TATTGAGAGT. This library was created for the University of Iowa Brain Anatomy Project (BMAP), 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
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ORIGIN

Query Match	46.8%;	Score 724;	DB 7;	Length 798;
Best Local Similarity	94.1%;	Pred. No. 4.2e-178;		
Matches 751; Conservative	0;	Mismatches 47;	Indels 0;	Gaps 0

Qy	16	CACAACTTTTCAGTGGCAAAATGCGACGTTATATGAAAAAGAAAGACCAAGCCAAAC	222
Db	1	CACAACTTCTCAGTGGCAAAATGCGACGTTATATGAAAAAGAAAGACCAAGCCAAATAC	60
Qy	223	ATTATTAATCAGATGCTTCAGGTGACTACTGTTATAGAGAAACATTTCAATGATAC	282
Db	61	ATTATTAATCAGATGCTTCAGGTGACCACTGTTATAGAGAAACATTTCAATGATAC	120
Qy	283	TCCAGAGGAAAGGAAAGATGACAGAAAGCTATCAGGCTGTAGCAACAGCTGCAGAG	342
Db	121	ACCAGAGGAAAGGAAAGGTGACCGAAGCTATCCAAAGCCGATCCAGCGATTCAGAG	180
Qy	343	GCAAGAGGAGAGAGATGGAATTTGATGCAACTTCACAAATTGATTAATAGAGAGA	402
Db	181	GCAAGAGGAGAGAGATGAATTTGATGCCCACTCAGATTAATTAATAGAGAGAGA	240
Qy	403	AGAGATGATGCTCTACACCCATCATMAAAGAAAGCAATGATATTTGACTATTT	462
Db	241	AGAGATGATGCTCTACACCCATCATMAAAGAAAGCAATGATATTTTGTACTATTT	300
Qy	463	GAAACTACTAGGTAAAGGCACTTTTGGGAAAGTTATTTGGTTGAGAGAAAGCAAGTGG	522
Db	301	GAAACTACTAGGTAAAGGCACTTTTGGGAAAGTTATTTGGTTGAGAGAAAGCAAGTGG	360
Qy	523	AAAATCTATGCTATGAAGATCTGGAAGAAAGATCAATTGTCAAAGATGAAAGTGG	582
Db	361	AAAATCTATGCTATGAAGATCTGGAAGAAAGATCTATTTGTCAAAGATGAAAGTGG	420
Qy	583	ACACACTCTAATGGAAGAGAGATTAAGAAAGACTAGACATCCCTTTTAAACATCTT	642
Db	421	ACACACTCTAATGGAAGAGATCTAAGAAAGCAACCAAGACATCATTTTAAACATCTT	480
Qy	643	GAATATTCCTTCAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGG	702

Db	Accession	Source	Organism	Reference Authors Title	Journal Comment	Features Source
Db	481	GAAATATTCCTTCAGACAAAAGACCGTTTGCTTTGTGTGATGGATATGTTAATGGCGG	540			
Qy	703	CGAGCTGTTTTTCCATTGTCGAGAGACCGGGTGTCTCTGAAGACCGCACCGTTTTCTA	762			
Db	541	AGAGCTGTTTTTCCATTGTCGAGAGACCGAGTGTCTCTGAAGACCGCACCGTTTTCTA	600			
Qy	763	TGTCGCAAAATTTGCTCGCGCTTGAGCATCTTACATTCGCGAAAGATTGTGTACCGCGA	822			
Db	601	TGTCGCAAAATTTGCTCGCTTGAGCATCTTACATTCGCGAAAGATTGTGTACCGCGA	660			
Qy	823	TCTCAAGTTGGAGATCTTAATGCTTGAGCAAAAGATGGCCACATTAATAATTCAGATTTTGG	882			
Db	661	TCTCAAGTTGGAGATTTGATGCTTATGATTAAGATGCGCATATTAATAATTCAGATTTTGG	720			
Qy	883	ACTTTGCAAGAGAGGATCAAGATGACGCCACCATGAAGACATTTCTGTGCACTCCAGA	942			
Db	721	GCTTTGCAAGAGAGGATCAAGATGACGATCAATGAAGACATTTCTGTGCAACACAGA	780			
Qy	943	ATATCTGCGACACAGGCT	960			
Db	781	GTACTGCGACACAGGCT	798			
RESULT 8	CA430499/c					
LOCUS	CA430499	785 bp	mRNA	linear	EST 07-NOV-2002	
DEFINITION	UI-H-FH1-bfc-c-24-0-UI.s1 NCI CGAP_FH1 Homo sapiens cDNA clone					
ACCESSION	UI-H-FH1-bfc-c-24-0-UI 3', mRNA sequence.					
VERSION	CA430499					
KEYWORDS	CA430499.1 GI:24793225					
SOURCE	EST.					
ORGANISM	Homo sapiens (human)					
REFERENCE	Homo sapiens					
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
JOURNAL	1 (bases 1 to 785)					
COMMENT	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .					
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),					
	Tumor Gene Index					
	Unpublished (1997)					
	Contact: Robert Strausberg, Ph.D.					
	Email: cgapbs-rt@mail.nih.gov					
	Tissue Procurement: James Martin					
	cDNA Library preparation: Dr. M. Bento Soares, University of Iowa					
	cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa					
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa					
	Clone Distribution: Clone distribution information can be obtained					
	from Dr. M. Bento Soares, bento-soares@iowa.edu					
	The following repetitive elements were found in this cDNA					
	sequence: 1-42, >AT-rich#low-complexity (matched complement)					
	Seq primer: M13 FORWARD					
	POLYA=yes.					
FEATURES	Location/Qualifiers					
source	1..785					
	/organism="Homo sapiens"					
	/mol_type="mRNA"					
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	/clone="UI-H-FH1-bfc-c-24-0-UI"					
	/tissue_type="Cell Line"					
	/dev_stage="Adult"					
	/lab_host="DH10B (Life Technologies)"					
	/clone_id="NCI CGAP_FH1"					
	/note="Organ: Chondrosarcoma; Vector: p7773-Pac					
	(Pharmacia) with a modified polylinker; Site 1: EcoR I;					
	Site 2: Not I; NCI CGAP FH1 is a normalized cDNA library					
	obtained from a cell line derived from grade I					
	chondrosarcoma tissue. The library was constructed and					
	normalized according to Bonaldo, Lennon and Soares, Genome					
	Research, 6:791-806, 1996. First strand cDNA synthesis was					
	performed with an oligo-dT primer containing a Not I site.					
	Double stranded cDNA was ligated to an EcoR I adaptor,					
	digested with Not I, and cloned directionally into					
	p7773-Pac vector. The oligonucleotide used to prime the					

synthesis of first-strand cDNA containing a library tag sequence that is located between the Not I site and the (dT)₁₈ tail. The sequence tag for this library is AGATCCGGC. The cell line was provided by Dr. James Martin from the University of Iowa.

TAG_TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1 Chondrosarcoma

TAG_LIB=UI-H-FH1

TAG_SEQ=AGATCCGGC"

Query Match	45.6%;	Score 705.8;	DB 6;	Length 785;
Best Local Similarity	96.6%;	Pred. No. 2.4e-173;		
Matches 719; Conservative	0;	Mismatches 25;	Indels 0;	Gaps 0;

OY		657	AGACAAAAGACCGTTGTGTTTTGGATGGAATAATGTAAATGGGGGCGAGCTGTTTTCC	716
Dd		785	AGA CAAAAGACCGTNTGTGTTTGTAATGTAAATGGGGGCGACTGTTTTTC	726
OY		717	ATTGTGCAGAGAGACGGGGTGTCTCTGAGACCGCACACGTTTCTAATGTGCAGAAATTG	776
Dd		725	ATTMTGTGAGAGAGACGGGGTGTCTCTGAGACCGCACACGTTTCTAATGTGCAGAAATTG	666
OY		777	TCTCTGCCCTTGGACTATCTACATTCCGGAAGAATGTGTACCCTGATCTCAAGTTGGAGA	836
Dd		665	TCTCTGCCCTTGGACTATCTACATTCGCCGAAGAATGTGTACCCTGATCTCAAGTTGGAGA	606
OY		837	ATTCTAATGCTGGACAAGAAATGGCCACATATAAAAAATTACAGATTTTGGACTTTGGCAAAG	896
Dd		605	ATCTAATGCTGGACAAGAAATGGCCACATATAAAAAATTACAGATTTTGGACTTTGGCAAAG	546
OY		897	GGATCACAAGATGCAACCCACCATGAGAATCTGTGTGCACTCCAGAATATCTGGCACAG	956
Dd		545	GGATCACAAGATGCAACCCACCATGAGAATCTGTGTGCACTCCAGAATATCTGGCACAG	486
OY		957	AGGTGTTAAGAAAGATAATGACTATATGGCCGAGCAGTACATGTGTGGGGCCTTAGGGGTGTCA	1016
Dd		485	AGGTGTTAAGAAAGATAATGACTATATGGCCGAGCAGTACATGTGTGGGGCCTTAGGGGTGTCA	426
OY		1017	TGTATGAAGATGATGTGGGAGGTGTACCTTCTTCAACAACGAGACCAATGAGAACTTTTTG	1076
Dd		425	TGTATGAAGATGATGTGGGAGGTGTACCTTCTTCAACAACGAGACCAATGAGAACTTTTTG	366
OY		1077	AATTATATTAATATGGAAGACATTAAATTTTCTCGAACACTCTCTTCAGATGCAAAATCAT	1136
Dd		365	AATTATATTAATATGGAAGACATTAAATTTTCTCGAACACTCTCTTCAGATGCAAAATCAT	306
OY		1137	TGCTTTCAAGGGCTCTTATTAAGGATTCGAAATTAACGCTTGGTGGAGAACCAATGATG	1196
Dd		305	TGCTTTCAAGGGCTCTTATTAAGGATTCGAAATTAACGCTTGGTGGAGAACCAATGATG	246
OY		1197	CAAAAGAAATTAATGAGACACAGTTTCTTCCTGAGATGAACCTGGCAAGATGTATATGATA	1256
Dd		245	CAAAAGAAATTAATGAGACACAGTTTCTTCCTGAGATGAACCTGGCAAGATGTATATGATA	186
OY		1257	AAAAGCTTGTAACCTCTTTTAAACCTTCAGATTAACATCTGAGACAGATACTAGATATTTTG	1316
Dd		185	AAAAGCTTGTAACCTCTTTTAAACCTTCAGATTAACATCTGAGACAGATACTAGATATTTTG	126
OY		1317	ATGAAGAATTTACAGCTCAAGCTATTTTCAATTAACCACTGAAAAAATATGATGAGAGATG	1376
Dd		125	ATGAAGAATTTACAGCTCAAGCTATTTTCAATTAACCACTGAAAAAATATGATGAGAGATG	66
OY		1377	GTAATGACCTGATGACCAATGAGAC	1400
Dd		65	ATTGTGGCAGTCTGTGGTAACCTGAH	42

RESULT 9
CN526558
LOCUS
DEFINITION

CN526558 776 bp mRNA linear EST 29-APR-2004
U1-M-HNO-con-d-20-0-U1.r1 NIH BMAP_HNO Mus musculus cDNA clone
IMAGE:30650491 5', mRNA sequence.

716
726
776
836
896
956
1016
1076
1136
1196
1256
1316
1376
66
1400
42

ACCESSION CN526558
 VERSION CN526558.1 GI:46854211
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 776)
 REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: csabbs-remail.nih.gov
 Tissue Procurement: Dr. James Ijz University of Iowa
 CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pYX-5.
 Location/Qualifiers
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 /note="Organ: Head; Vector: pYX-Asc; Site: 1: Ecor I;
 Site 2: Not I; The library was constructed according
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with Ecor I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is CGACTGAT. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH)."

ORIGIN

Query Match 45.6%; Score 704.8; DB 7; Length 776;
 Best Local Similarity 95.0%; Pred. No. 4,4e-173;
 Matches 738; Conservative 0; Mismatches 38; Indels 1; Gaps 1;

37 AGGTGGGTCAGAGAGGAGAGATATATATAAACTGGAGGCCAAGATCTTCCTTT 96
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 Db 1 AGGTGGGTCAGAGAGGAGAGATATATATAAACTGGAGGCCAAGATCTTCCTTT 60
 |||||
 QY 97 GAAGACAGATGGCTCATTCATAGATATTAAGAAAACCTCAAGATGTGGATTACCTTA 156
 |||||
 Db 61 GAAGACAGATGGCTCATTCATAGATATTAAGAAAACCTCAAGATGTGGATTACCTTA 120
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 QY 157 TCCCTTCACAACTTTTCAGTGGCAAAATCCGATTATATAAAACGAGACCAAGCC 216
 |||||
 Db 121 TCCCTTCACAACTTTTCAGTGGCAAAATCCGATTATATAAAACGAGACCAAGCC 180
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 QY 217 AACACATTTATATCATGATGTCTCCAGTGAAGCTACTGTTATAGAGAACTTTCATGT 276
 |||||
 Db 181 AAATACATTTATATCATGATGTCTCCAGTGAAGCTACTGTTATAGAGAACTTTCATGT 240
 |||||
 QY 277 AGATTAATCCAGAGAAAGGAGAAATGAGACAGAGCTATCCAGCTGTGTAGCAGACACT 336
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 Db 241 AGATTAATCCAGAGAAAGGAGAAATGAGACAGAGCTATCCAGCTGTGTAGCAGACACT 300
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QY 337 GCAGAGCAAGAAAGAGAGAGATGAAATTGATGCCAATTCACAAATTGATATATAGG 396
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 Db 301 GCAGAGCAAGAAAGAGAGAGATGAAATTGATGCCAATTCACAAATTGATATATAGG 360
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 QY 397 AGAGAAAGATGATGATGCTCTTACAAACCATCATTAAGAAAGACAAATGATTTTGA 456
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 Db 361 AGAGAAAGATGATGATGCTCTTACAAACCATCATTAAGAAAGACAAATGATTTTGA 420
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 QY 457 CTATTGAAACCTATGATGATTAAGGACCTTTGGGAAAGTTATTTTGGTCGAGAAAGC 516
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 Db 421 CTATTGAAACCTATGATGATTAAGGACCTTTGGGAAAGTTATTTTGGTCGAGAAAGC 480
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 QY 577 AGTGACACACACTCTACTAGTAAAGACAGAGATTTAAAGACATGACATCCCTTTTAA 636
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 Db 541 AGTGACACACACTCTACTAGTAAAGACAGAGATTTAAAGACATGACATCCCTTTTAA 600
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 QY 637 ATCTTGAAGATATCTCTTCCAGCAAAAGACCGTTTGTGTTTGTATGATATATTTA 696
 |||||
 Db 601 ATCTTGAAGATATCTCTTCCAGCAAAAGACCGTTTGTGTTTGTATGATATATTTA 660
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 QY 697 TGGGGCGAGCTGTTTTCATTTGCGAGAGCGGGTCTCTGAGGACCGCACAG 756
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 Db 661 TGGGGCGAGCTGTTTTCATTTGCGAGAGCGGGTCTCTGAGGACCGCACAG 720
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 QY 757 TTCTTATGATGAGAAATGTCCTCTGAGATCTATCTTCCGAGAAAGATTTGT 813
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 Db 721 TTCTTATGATGAGAAATGTCCTCTGAGATCTATCTTCCGAGAAAGATTTGT 776
 |||||

RESULT 10
 AK040758
 LOCUS
 DEFINITION
 Mus musculus adult male aorta and vein cDNA, RIKEN full-length
 enriched library, clone:R530023F15 product:chymoma viral
 proto-oncogene 1, full insert sequence.
 AK040758
 VERSION AK040758.1 GI:26333954
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 REFERENCE
 AUTHORS Carinci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 2
 REFERENCE
 AUTHORS Carinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subfraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 2049374
 PUBMED 11042159
 3
 REFERENCE
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Saeki, N., Carinci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Taisho, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

RESULT	12
BUT03964	
LOCUS	BUT03964
DEFINITION	BUT03964 766 bp mRNA linear EST 15-JUL-2003
UI-M-F00-bzr-i-04-0-UI.r1 NIH BMAP_F00 Mus musculus cDNA clone IMAGE:6406347 5' , mRNA sequence.	
ACCESSION	BUT03964
VERSION	BUT03964.1 GI:23631576
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction. Ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemm Chih, Ph.D., program coordinator."

ORIGIN

Query Match 44.8%; Score 695; DB 6; Length 759;
Best Local Similarity 94.7%; Pred. No. 1.6e-170;
Matches 719; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 91 CCTTTGAGACAGATGGCTCATTCATAGATATTAAGAGAAACCTCAGATGTGATTT 150
Db 1 CCTTTGAGACAGATGGCTCATTCATAGATATTAAGAGAAACCTCAGATGTGACTT 60

QY 151 ACCTTATCCCTCTCAACACTTTTCAGTGGCAAAATGCCAGTTAATGAAAACAGACACC 210
Db 61 ACCTTATCCCTCTCAACACTTTTCAGTGGCAAAATGCCAGTTAATGAAAACAGACACC 120

QY 211 AAGCCAAACACATTTATATCAGATGCTCCAGTGGACTACTGTTATAGAGAAACATT 270
Db 121 AAGCCAAACACATTTATTCAGATGCTTCAGTGGACCACTGTTATAGAGAAACATT 180

QY 271 TCATGTAGATATCTCCAGAGAAAGGAGAGATGAGACAGAACTATCCAGGCTGAGACA 330
Db 181 TCATGTAGATATCACAGAGAGAAAGAGAGATGAGACAGAACTATCCAGGCTGAGACA 240

QY 331 CAGACTGCAGAGGCAAGAGAGAGAGATGATTTGATGCTCAACTTCACAAATTTGATA 390
Db 241 CCATTTGCAGAGGCAAGAGAGAGAGATGATTTGATGCTCAACTTCACAAATTTGATA 300

QY 391 TATAGAGAGAGAGATGATGCTCTACACCCATCATTAAGAGAAAGCAATGATGA 450
Db 301 TATAGAGAGAGAGATGATGCTCTACACCCATCATTAAGAGAAAGCAATGATGA 360

QY 451 TTTTGAATTTTGAACCTAGATTAAGGCACTTTTGGAAAGTTATTTGGTTGAGACA 510
Db 361 TTTTGAATTTTGAACCTAGATTAAGGCACTTTTGGAAAGTTATTTGGTTGAGACA 420

QY 511 GAAGGCAAGTGAAGAAATCTATGCTATGAAGATTTGAGAGAAAGAGCTATTTGCAAA 570
Db 421 GAAGGCAAGTGAAGAAATCTATGCTATGAAGATTTGAGAGAAAGAGCTATTTGCAAA 480

QY 571 GGATGAAGTGGCAGACCTCTAATCTGAAGAGATTTAAGAACTAGACATCCCTT 630
Db 481 GGATGAAGTGGCAGACCTCTAATCTGAAGAGATTTAAGAACTAGACATCCCTT 540

QY 631 TTTAACAATCCTTGAATAATATCTTCCAGACAAAAGCCGTTTGTGTTTGTGATGATA 690
Db 541 TTTAACAATCCTTGAATAATATCTTCCAGACAAAAGCCGTTTGTGTTTGTGATGATA 600

QY 691 TGTTAATGGGGGAGAGCTGTTTTCATTTGTCAGAGAGACGGGCTTCTTGAAGACCG 750
Db 601 TGTTAATGGGGGAGAGCTGTTTTCATTTGTCAGAGAGACGGGCTTCTTGAAGACCG 660

QY 751 CACACGTTCTATGGGCAAAATGTCCTGCTTGGAGCTATCTACATTTGGAAGAT 810
Db 661 CACACGTTCTATGGGCAAAATGTCCTGCTTGGAGCTATCTACATTTGGAAGAT 720

QY 811 TGTGTACCGTATCTCAAGTTGAGAGATCTAATGCTGGA 849
Db 721 TGTGTACCGTATCTCAAGTTGAGAGATTTGATGCTAGA 759

RESULT 14
CK639280 760 bp mRNA linear EST 28-JAN-2004
LOCUS CK639280
DEFINITION UT-M-H00-cmx-d-16-0-UT.r1 NIH_BMAP_H00 Mus musculus cDNA clone

IMAGE:30637815 5', mRNA sequence.
CK639280
VERSION CK639280.1 GI:41365146
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE NIH-MGC <http://mgi.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mouse1.html>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES
source

Seq primer: pYX-5.
Location/Qualifiers
1..760
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30637815"
/rname_type="Upper Head"
/dev_stage="9.5-10.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_11b="NIH BMAP H00"
/note="Organ: Head; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction. Ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGACTGAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

ORIGIN

Query Match 44.8%; Score 692.8; DB 7; Length 760;
Best Local Similarity 94.5%; Pred. No. 6e-170;
Matches 718; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 195 TGAAGACAGACCAAGCCAAACACATTTATATCAGATGCTCCAGTGAATCACTAC 254
Db 1 TGAAGACAGACCAAGCCAAACACATTTATATCAGATGCTCCAGTGAATCACTAC 60

QY 255 TTATAGAGAGACATTTCAATGATATCTCCAGAGAGAGAGAGATGAGACAGAGCTA 314
Db 61 TTATAGAGAGACATTTCAATGATATCTCCAGAGAGAGAGAGATGAGAGAGAGCTA 120

QY 315 TCCAGGCTGTAGACAGACAGCTGACAGAGCAAGAGAGAGAGATGAATTTGATGCCA 374
Db 121 TCCAGGCTGTAGAGCCAGCCAGATTCAGAGAGCAAGAGAGAGAGATGAATTTGATGCCA 180

QY 375 CTTCACAAATTTATATATATAGAGAGAGAGAGATGATGCTCTTAACCCATCAATAAA 434
Db 181 CTTCACAGATGATATATATATATAGAGAGAGAGATGATGCTCTTAACCCATCAATAAA 240

QY 435 GAAAGCAATGATGATTTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 494
Db 241 GAAAGCAATGATGATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 300

QY 495 TTATTTGGTTCAGAGAGGCAAGTGAATACTATGTAAGATTCTGAAGAG 554
 DB 301 TTATTTGGTTCAGAGAGGCAAGTGAATACTATGTAAGATTCTGAAGAG 360
 QY 555 AAGTCTATTGTAAGAGATGAAGTGGCACACTCTTAACGTAAGACAGATTAAGA 614
 DB 361 AAGTCTATTGTAAGAGATGAAGTGGCACACTCTTAACGTAAGACAGATTAAGA 420
 QY 615 ACACATGACATCCCTTTTAACATCCTTGAATAATCTCTCCAGACAAAGCCGTTGT 674
 DB 421 AACCCAGATTCATTTTAACTATGTAAGTCTTGAAGATTAAGACAGACAGACGTTGT 480
 QY 675 GTTTTGTGATGAATATGTTAATGAGGAGAGCTGTTTTCCATTGTGAGAGAGCGG 734
 DB 481 GTTTTGTGATGAATATGTTAATGAGGAGAGCTGTTTTCCATTGTGAGAGAGCGG 540
 QY 735 TGTTCCTGAGAGCCGACACGTTTCTATGAGTGCAGAAATGTTCTGCTTGACTATC 794
 DB 541 TGTTCCTGAGAGCCGACACGTTTCTATGAGTGCAGAAATGTTCTGCTTGACTATC 600
 QY 795 TACATTCGGGAAGATTGTTACCGTATCTCAAGTTGAGATCTAATGCTGAGACAAG 854
 DB 601 TACATTCGGGAAGATTGTTACCGTATCTCAAGTTGAGATCTAATGCTGAGACAAG 660
 QY 855 ATGGCCACATTAATAATTAAGATTTTGAATTTGCAAAAGAGGATCAGAGATGACGCA 914
 DB 661 ATGGCCATTAATAATAATTAAGATTTTGGGCTTTGCAAAAGAGGATCAGAGATGACGCA 720
 QY 915 CCATGAAGACATTTCTGTGCACTCCAGAAATATTTGCGACC 954
 DB 721 CCATGAAGACATTTCTGTGCACTCCAGAGATCCTGCGACC 760

RESULT 15
 LOCUS CB525973 746 bp mRNA linear EST 09-JUL-2003
 DEFINITION UI-M-FY0-cfb-h-05-0-UI.x1 NIH_BMAP_FY0 Mus musculus cDNA clone
 ACCESSION CB525973 IMAGE:6847254 5', mRNA sequence.
 VERSION CB525973.1 GI:29359446
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 746)
 NIH-MGC <http://mgc.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouseefi.html>
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES
 source
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:6847254"
 /issue_type="whole brain"
 /dev_stage="embryo 13.5, 14.5, 16.5, 17.5 dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_FY0"
 /note="Organ: Brain; Vector: pYX-Asc; Site_1: Ecor I;

Seq primer: pYX-5.
 Location/Qualifiers
 1..746
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:6847254"
 /issue_type="whole brain"
 /dev_stage="embryo 13.5, 14.5, 16.5, 17.5 dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_FY0"
 /note="Organ: Brain; Vector: pYX-Asc; Site_1: Ecor I;

Site 2: Not I; The library was constructed according to Bonaldo, Lemmon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with NotI and then cloned directionally into pYX-Aec vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): "Gene Discovery in the Developing Mouse Nervous System", supported by National Institute of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 43.8%; Score 677.4; DB 6; Length 746;
 Best Local Similarity 94.2%; Pred. No. 6; Se-166;
 Matches 702; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 129 AGAAGCTCAAGATGATGATTAACCTTATCCCTCAACAACTTTCAAGTGGCAATGCC 188
 DB 1 AGAAGCTCAAGATGATGATTAACCTTATCCCTCAACAACTTTCAAGTGGCAATGCC 60
 QY 189 AGTTAATGAAACAGAACGACCAAGCCAAACATTTAATAGATGCTCCAGTGA 248
 DB 61 AGTTAATGAAACAGAACGACCAAGCCAAATTAATTAATAGATGCTCCAGTGA 120
 QY 249 CTACTGTTTATAGAGAACTTTCAATGATTAATCTCCAGAGAAAGGAAATGACAG 308
 DB 121 CCAGTGTATTAAGAGAACATTTCAATGATTAATCAACAGAGAAAGAGTGAACG 180
 QY 309 AAGCTATCCAGGCTGAGAGACAGACAGCTGACAGAGCAAGAAAGAGAGATGATTTGA 368
 DB 181 AAGCTATCCAGGCTGAGAGACAGACAGCTGACAGAGCAAGAGAGATGATTTGA 240
 QY 369 GTCCAACTTCACAAATGATTAATATAGAGAGAAAGAGATGATGATCTTACACCCATC 428
 DB 241 GCCCAACCTTCACAGATGATTAATATAGAGAGAAAGAGATGATGATGATCAACCCATC 300
 QY 429 ATTAAGAAAGACATGATGATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 488
 DB 301 ATTAAGAAAGACATGATGATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 360
 QY 489 GGAAGTATTTTGGTTCAGAGAGAGCAAGTGAATACTATGCTATGAGATTTCTGA 548
 DB 361 GGAAGTATTTTGGTTCAGAGAGAGCAAGTGAATACTATGCTATGAGATTTCTGA 420
 QY 549 AGAAGAACTCATTTATGCAAGATGAAGTGGCACACTCTTAACGTAAGACAGATAT 608
 DB 421 AGAAGAACTCATTTATGCAAGATGAAGTGGCACACTCTTAACGTAAGACAGATAT 480
 QY 609 TAAAGAACCTAGACATCCCTTTTAACTCTTGAATATTTCTTCCAGACAAAGACC 668
 DB 481 TAAAGAACCTAGACATCCCTTTTAACTCTTGAATATTTCTTCCAGACAAAGACC 540
 QY 669 GTTTGTTTGTGATGATGATTAATGAGGAGAGAGCTGTTTTCCATTGTGAGAG 728
 DB 541 GTTTGTTTGTGATGATGATTAATGAGGAGAGAGCTGTTTTCCATTGTGAGAG 600
 QY 729 AGCGGATGTTCTGAGAGACGACACGTTTCTATAGTGCAGAAATGTTCTGCTGCTGG 788
 DB 601 AGCGGATGTTCTGAGAGACGACACGTTTCTATAGTGCAGAAATGTTCTGCTGCTGG 660
 QY 789 ACTATCTACATTCGGAAGATTTGTGATCCGATCTCAAGTTGGAATCTTAAGCTGG 848
 DB 661 ACTATCTACATTCGGAAGATTTGTGATCCGATCTCAAGTTGGAATCTTAAGCTGG 720
 QY 849 ACAAGAGGCGACATTAATAATTAC 873
 DB 721 ATTAAGAGGCGCATTAATAATTAC 745

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Job time : 4728 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: April 13, 2005, 06:12:34 ; Search time 5103 Seconds
(without alignments)
4346.314 Million cell updates/sec

Title: US-09-869-079b-3

Perfect score: 2558

Sequence: 1 MSDVITVKEGWQKGEYIK.....MNERRPHPPQSYASGRE 479

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb_hc:.*
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12: gb_sy:.*
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14: gb_vl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2558	100.0	1440	BD142211	BD142211 Method to
2	2558	100.0	1440	12 AY335691	AY335691 Synthetic
3	2558	100.0	1547	6 BD251226	BD251226 Human Akt
4	2558	100.0	1547	6 AX026529	AX026529 Sequence

5	2558	100.0	1547	9 HSA245709	AJ245709 Homo sapi
6	2558	100.0	1706	9 AF085234	AF085234 Homo sapi
7	2558	100.0	1708	9 AF124141	AF124141 Homo sapi
8	2558	100.0	2367	6 BD260777	BD260777 Human pro
9	2558	100.0	2811	9 AF135794	AF135794 Homo sapi
10	2545	99.5	1436	6 BD251227	BD251227 Human Akt
11	2545	99.5	1436	6 AX026530	AX026530 Sequence
12	2543	99.4	1760	10 AF124142	AF124142 Mus muscu
13	2533	99.0	4751	10 BC066861	BC066861 Mus muscu
14	2480	97.0	1551	6 CQ714620	CQ714620 Sequence
15	2402	93.9	1570	6 BD250154	BD250154 AKT nucle
16	2402	93.9	1570	6 AX056819	AX056819 Sequence
17	2402	93.9	1570	6 AX251592	AX251592 Sequence
18	2402	93.9	1584	9 HSM801048	AL117525 Homo sapi
19	2402	93.9	1595	9 AY005799	AY005799 Homo sapi
20	2386	93.3	1548	10 RARACPCG	D49836 Rat mRNA fo
21	2146.5	83.9	2277	5 AF039943	AF039943 Gallus ga
22	2113	82.6	1608	5 AF317656	AF317656 Xenopus 1
23	2105.5	82.3	1443	12 AY335629	AY335629 Synthetic
24	2105.5	82.3	2729	9 BC000479	BC000479 Homo sapi
25	2105.5	82.3	2688	9 BC084538	BC084538 Homo sapi
26	2105.5	82.3	3410	9 HSM808353	BX648205 Homo sapi
27	2100.5	82.1	2626	6 BD270825	BD270825 AKT compo
28	2100.5	82.1	2626	6 AR474029	AR474029 Sequence
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32	2099.5	82.1	1443	6 BD142209	BD142209 Method to
33	2099.5	82.1	2181	6 A84455	A84455 Sequence 70
34	2099.5	82.1	2181	6 CQ829979	CQ829979 Sequence
35	2099.5	82.1	2181	6 AR279918	AR279918 Sequence
36	2099.5	82.1	2181	6 AX427354	AX427354 Sequence
37	2099.5	82.1	2181	6 BD082540	BD082540 A method
38	2099.5	82.1	2184	6 A84523	A84523 Sequence 13
39	2099.5	82.1	2184	6 CQ830047	CQ830047 Sequence
40	2099.5	82.1	2184	6 AR279966	AR279966 Sequence
41	2099.5	82.1	2184	6 AX427422	AX427422 Sequence
42	2099.5	82.1	2184	6 BD082568	BD082568 A method
43	2099.5	82.1	2610	6 A62733	A62733 Sequence 1
44	2099.5	82.1	2610	6 A63232	A63232 Sequence 3
45	2099.5	82.1	2610	6 AR076381	AR076381 Sequence

ALIGNMENTS

RESULT 1
BD142211
LOCUS
DEFINITION Method for controlling apoptosis and polypeptide controlling
ACCESSION BD142211.1 GI:223237156
VERSION BD142211.1
KEYWORDS WO 0215925-A/5.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1440)
Tsurno, T., Fujita, N. and Sato, S.
TITLE Method for controlling apoptosis and polypeptide controlling
JOURNAL Patent: WO 0215925-A 5 28-FEB-2002;
KYOWA HAKKO KOGYO CO LTD, TAKASHI TSURNO, NAOYA FUJITA, SAORI SATO
OS Homo sapiens (human)
PN WO 0215925-A/5
PD 28-FEB-2002
PF 22-AUG-2001 WO 2001JP007179
PI 22-AUG-2000 JP 00P 251529
PC TAKASHI TSURNO, NAOYA FUJITA, SAORI SATO
PC A61K38/17, A61K38/45, A61K39/395, A61K45/00, A61P43/00, A61P3/08,
PC A61P43/00, C07K7/04, C07K14/47, C07K16/18, C12N1/15, C12N1/19 PC
C12N1/21, C12N5/10,
PC C12P21/02, C12N15/09, G01N33/50, G01N33/15, G01N33/566, G01N33/58

FEATURES
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 FT source
 Location/Qualifiers
 1..1440
 /organism='Homo sapiens (human)'
 /mol_type='genomic DNA'
 /db_xref='taxon:9606'

ALIGNMENT SCORES:

Pred. No.: 3,73e-213 Length: 1440
 Score: 2558.00 Matches: 479
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-09-869-079B-3 (1-479) x BD142211 (1-1440)

QY 1 MetSerAspValThrIleValIysGluIYTPVAlGlnLysArgGlyGluTyrIleLys 20
 DB 1 ATGAGCGATGTTACCATTTGAAAGAGGTGGGTTCAAGAGGGGAGAAATATATAA 60
 QY 21 AenTPARProARgTYrPheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGlu 40
 DB 61 AACTGAGGCCAAGACTTCCTTTGAAAGACAGATGGCTCATTCATAGATATAAGAG 120
 QY 41 LysProGlnAspValAspLeuProTYrProLeuAsnAsnPheserValAlaLysCysGln 60
 DB 121 AAACCTCAAGATGTGATTACCTTATCCCTCAACACTTTTCAGTGGCAAAATGCCAG 180
 QY 61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTPMtr 80
 DB 181 TTAAATGAAGACAGAGACCAAGCAACCAATTAATATCATGATGTCCTCAGTGGACT 240
 QY 81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluIUTrPThrGlu 100
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 QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgLysMetLysCysSer 120
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 QY 421 ProPheLysProGluValThrSerGluThrAspTrpArgTYrPheAspGluGluPheThr 440
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 DEFINITION
 Synthetic construct Homo sapiens v-akt murine thymoma viral oncogene-like 3 (AKT3) mRNA, partial cds.
 ACCESSION
 AY335691
 VERSION
 AY335691.1 GI:33304020
 KEYWORDS
 FLI CDNA.
 SOURCE
 synthetic construct
 ORGANISM
 other sequences; artificial sequences.
 1 (bases 1 to 1440)
 2 (bases 1 to 1440)
 TITLE
 Cloning of human full-length CDS FLEXGene kinases in recombinational vector system
 JOURNAL
 Park,J., Rolfe,A., Hu,Y., Shen,B., Vannberg,F., Moreira,D., Kelley,T., Zuo,D., Raphael,J., Baqui,M., Jepson,D., Harlow,E., Labaer,J., and Brizuela,L.
 Direct Submision
 Submitted (02-JUN-2003) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141-2023, USA
 This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics.
 Each CDS has been cloned without stop-codon (to allow fusion with

C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame.

FEATURES

source

Location/Qualifiers
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CDS

gene

ORIGIN

Alignment Scores:

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-869-079B-3 (1-479) x AY335691 (1-1440)

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41 LysPProGlnAspValAspLeuProTYrProLeuAsnAsnPheSerValAlaIysCysGln 60
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301 GCATTCAGAGCTGTACAGACAGACTGCAGAGGCAAGAGAGGAATGAAATGTGTAGT 360
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901 GCCACCATTAAGACATTCGTGTGCACTCCAGATATCTGGCACAGAGGTGTTAAGAGAT 960
321 AsnAspTYrGlyArGAlaValAspTPrPrgIlyLeuGlyValIleMetTYrGluMetMet 340
961 AATGACTATGGCGGAGCAGTAGACTGTGGGGCCCTAAGGGGTGTCATGATATAATGAG 1020
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1321 GCTCAGACTATTAACATTAACACACCTGAAATATGATGAGATGTGTGACTGCAATG 1380
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BD251226
LOCUS BD251226 1547 bp DNA linear PART 17-JUL-2003

DEFINITION Human Akt-3.
ACCESSION BD251226
VERSION BD251226.1 GI:33060996
KEYWORDS JP 2002535964-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1547)
AUTHORS Masure, S.L.J. and Richardson, A.
TITLE Human Akt-3.
JOURNAL Patent: JP 2002535964-A 1 29-OCT-2002;
JANSSEN PHARMA/CEUTICA NV
OS Homo sapiens (human)
PN JP 2002535964-A/1
PD 29-OCT-2002
PF 17-DEC-1999 JP 2000589669
PR 22-DEC-1998 GB 9828375.7
PI STEFAN LEO JOZEF MASURE, ALAN RICHARDSON
PC C12N15/09, A61K31/713, A61K38/53, A61K39/395, A61K39/395, A61K48/00, PC
A61P35/00.
PC A61P43/00, C07K16/40, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/
PC 12, C12Q1/02,
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Score: 2558.00 Matches: 479
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-869-079B-3 (1-479) x BD251226 (1-1547)

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AX026529

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 VERSION AX026529.1 GI:10187717
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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 1 Masure, S.L. and Richardson, A.
 AUTHORS Human akt-3
 TITLE Patent: WO 003613-A 1 29-JUN-2000:
 JOURNAL MASURE STEPHAN LEO JOZEF (BR) ; RICHARDSON ALAN (BE) ; JANSSEN PHARMACEUTICA NV (BE)
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 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
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 US-09-869-079B-3 (1-479) x AX026529 (1-1547)

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 DEFINITION Homo sapiens mRNA for serine/threonine kinase Akt-3 (Akt3 gene).
 ACCESSION AJ245709
 VERSION AJ245709.1 GI:5804885
 KEYWORDS Akt-3; Akt3 gene.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 Masure, S., Haefner, B., Weselink, J.J., Hofnagel, E., Mortier, E.,
 Verhaesele, P., Tytelers, A., Gordon, R. and Richardson, A.
 TITLE Molecular cloning, expression and characterization of the human
 serine/threonine kinase Akt-3
 JOURNAL Eur. J. Biochem. 265 (1), 353-360 (1999)
 MEDLINE 99421751

PUBMED 10491192
REFERENCE 2 (bases 1 to 1547)
AUTHORS Masure S.L.
TITLE Direct Submission
JOURNAL Submitted (25-AUG-1999) Masure S.L., Biotechnology & High-Throughput Screening, Janssen Research Foundation, Turnhoutseweg 30, B-2340 Beerse, BELGIUM
COMMENT Phosphorylation at Thr305 and at Ser472 necessary for activation.
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ACCESSION AF085234
VERSION AF085234.1 GI:17529662
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1706)
Li, X., Yu, L., Huang, H., Zhang, M., Zhao, Y. and Zhao, S.
Cloning of a novel human cDNA, STR-2, which encodes a rat
serine-threonine protein kinase (STR) homolog
Unpublished
JOURNAL 2 (bases 1 to 1706)
Zhao, Y.
AUTHORS Direct Submission
TITLE Submitted (22-AUG-1998) Zhao Y., Institute of Genetics, Fudan
University, Lab of Human Gene Research, No. 220, Handan Road,
Shanghai, People's Republic of China, 200433
JOURNAL Location/Qualifiers
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US-09-869-079b-3 (1-479) x AF085234 (1-1706)

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ACCESSION AF124141
VERSION AF124141.1 GI:4757578
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1708)
AUTHORS Brodebeck,D., Cron,P. and Hemmings,B.A.
TITLE A human protein kinase Bgamma with regulatory phosphorylation sites
in the activation loop and in the C-terminal hydrophobic domain
JOURNAL J. Biol. Chem. 274 (14), 9133-9136 (1999)
MEDLINE 99194749
PUBMED 10092583
REFERENCE 2 (bases 1 to 1708)
AUTHORS Brodebeck,D., Cron,P. and Hemmings,B.A.
TITLE Direct Submission
JOURNAL Submitted (27-JAN-1999) Friedrich Miescher-Institut,
Maulbeerallee 66, Basel 4058, Switzerland
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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US-09-869-079B-3 (1-479) x AF124141 (1-1708)

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AF135794
LOCUS Homo sapiens AKT3 protein kinase mRNA, complete cds.
DEFINITION AF135794
ACCESSION AF135794
VERSION AF135794.1 GI:4574743
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2811)
Nakatani, K., Sakaue, H., Thompson, D.A., Weigel, R.J. and Roth, R.A.
TITLE Identification of a human AKT3 (protein kinase B gamma) which
contains the regulatory serine phosphorylation site
JOURNAL Biochem. Biophys. Res. Commun. 257 (3), 906-910 (1999)
MEDLINE 99225329
PUBMED 10208883
REFERENCE 2 (bases 1 to 2811)
Thompson, D.A., Nakatani, K. and Sakaue, H.
TITLE Direct Submission
JOURNAL Submitted (18-MAR-1999) Surgery, SMLS Building, Room P228, 1201
Welch Road, Stanford, CA 94305, USA
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ORIGIN
Alignment Scores:
Pred. No.: 8.17e-213 Length: 2811
Score: 2558.00 Matches: 479
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-869-079B-3 (1-479) x AF135794 (1-2811)

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LOCUS BD251227 Human Akt-3.
DEFINITION BD251227
ACCESSION BD251227.1 GI:33060997
VERSION JP 2002535964-A/2.
KEYWORDS JP 2002535964-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1436)
AUTHORS Masure,S.L.J. and Richardson,A.
JOURNAL Human Akt-3
Patent: JP 2002535964-A 2 23-OCT-2002;
JANSSEN PHARMACEUTICA NV
OS Homo sapiens (human)
COMMENT PN JP 2002535964-A/2
PD 29-OCT-2002 JP 2000589669
PF 17-DEC-1999 JP 2000589669
PR 22-DEC-1998 GB 9828375.7
PI STEFAN LEO JOZEF MASURE,ALAN RICHARDSON
PC C12N15/09,A61K31/713,A61K38/53,A61K39/395,A61K39/395,A61K48/00,PC
A61P35/00,
PC A61P43/00,C07K16/40,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
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FH Key
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Best Local Similarity: 99.79% Mismatches: 1
Query Match: 99.49% Indels: 0
DB: 6 Gaps: 0
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LOCUS Sequence 2 from Patent WO0037613.
DEFINITION AX026530
ACCESSION AX026530
VERSION AX026530.1 GI:10187718
KEYWORDS
SOURCE
ORGANISM
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
1 Masure, S.L. and Richardson, A.
Human akt-3
Patent: WO 0037613-A 2 29-JUN-2000,
MASURE STEFAN LEO JOZEF (BE) ; RICHARDSON ALAN (BE) ; JANSSEN
PHARMACEUTICA NV (BE)

FEATURES
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Location/Qualifiers
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Score: 2545.00 Matches: 477
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Query Match: 99.49% Indels: 0
DB: 6 Gaps: 0

US-09-869-079B-3 (1-479) x AX026530 (1-1436)

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1417 GACAAACGAGCGGCGGACACATCTCCCTCAGTTCTCTACTCTGCAAGCGGAGAA 1473

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LOCUS BC066861 4751 bp mRNA linear ROD 30-JUN-2004

DEFINITION Mus musculus thymoma viral proto-oncogene 3, mRNA (cDNA clone

ACCESSION BC066861

VERSION BC066861.1 GI:45219866

KEYWORDS MGC.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 4751)

AUTHORS Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buecaw, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.F., Rubin, G.M., Hong, L., Stalderon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carmin, R.P., Prange, C., Raha, S.S., Loggellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Huijks, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 4751)

Strausberg, R.

Direct Submission

Submitted (01-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

Contact: MGC help desk

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Dr. Angelo L. Vescovi (Institute for Stem Cell Research, Italy)

cDNA Library Preparation: Yulan Piao and Minoru Ko (National Institute on Aging, NIH: <http://lgsun.grc.nia.nih.gov/cDNA/>)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: <http://www-ehg.stanford.edu>

Contact: (Dickson, Mark) mcdbpax1.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>

Series: IRAK Plate: 144 Row: e Column: 13

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6753031.

Location/Qualifiers

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ORIGIN

Alignment Scores:

Pred. No.: 2,276-210 Length: 4751

Score: 2533.00 Matches: 475

Percent Similarity: 99.58% Conservative: 2

Best Local Similarity: 99.16% Mismatches: 0

Query Match: 99.02% Indels: 0

Gaps: 0

US-09-869-079B-3 (1-479) x BC066861 (1-4751)

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Db 287 ACTGTTATAGAGAAACATTTTCATATATATACACAGAGAGAAAGAGATGACGAGAA 346

Qy 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnIuTyGluArgMetAsnCysSer 120

Db 347 GCTATCAAGCGGTGACGACCGATTCAGAGGCAAGAGAGAGATGATGATTTGTAGC 406

Qy 121 ProThrSerGlnIleAspAsnIleGlyGluGluIuTyMetAspAlaSerThrThrHis 140

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QY 296 GlyIleThrAspAlaIleThrMetLeuTyrPhePheGlyTyrProGluTyrLeuAlaPro 315
DB 841 GGGATCAGAGATGACACCCACACATGAGACATTTCTGCGCATCTCCAAATATCTCGSACA 900
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ACCESSION BD250154
VERSION BD250154.1 GI:33059924
KEYWORDS JP 2002539781-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Guo,K., Pagnoni,M.F., Clark,K.L. and Ivashchenko,Y.D.
AKT nucleic acids, polypeptides, and uses thereof
Patent: JP 2002539781-A 1 26-NOV-2002;
AVENTIS PHARMACEUTICALS PRODUCTS INC
OS Homo sapiens (human)
PN JP 2002539781-A/1
PD 26-NOV-2002
PF 14-MAR-2000 JP 2000606725

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PR 19-MAR-1999 US 60/125108
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Query Match: 93.90% Indels: 2
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DB 606 AAAGTATTTTGTGTCGAGAGAGAGCAAGTGAAGAAATACTATGCTATGAAGATTCTGAAG 665
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Job time : 5130 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 13, 2005, 04:22:03 ; Search time 644 Seconds
(without alignments)

4403.037 Million cell updates/sec

Title: US-09-869-079B-3

Perfect score: 2558
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsun62 -TRANS=humand.0.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	2558	100.0	2367	3	AAC61592	Aac61592 DNA encod

6	2558	100.0	2811	10	ADC26888	Adc26888 DNA encod
7	2558	100.0	2811	13	ADQ88265	Adq88265 Human 141
8	2550	99.7	3285	3	AAC77341	Aac77341 Human ORF
9	2402	93.9	1570	3	AAA96637	Aaa96637 DNA encod
10	2402	93.9	1570	4	AAH79025	Aah79025 Human Akt
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13	2465	83.9	2277	12	ADN71941	Adn71941 Chicken s
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15	2405.5	82.3	2978	9	ACD44893	Acd44893 Human sig
16	2400.5	82.1	2626	3	AAa09078	Aa09078 Wild type
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19	2400.5	82.1	2626	12	ADP48780	Adp48780 Mouse Akt
20	2400.5	82.1	6891	12	ADL25356	Adl25356 ARKs re1a
21	2099.5	82.1	1443	6	ABLS0837	Ab150837 Human Akt
22	2099.5	82.1	1443	10	ADP18631	Adp18631 Human Akt
23	2099.5	82.1	2181	2	AAV71037	Aav71037 PKB-green
24	2099.5	82.1	2184	2	AAV71086	Aav71086 Green flu
25	2099.5	82.1	2610	2	AAE67135	Aae67135 Human RAC
26	2099.5	82.1	2610	2	AAE64812	Aae64812 Human RAC
27	2099.5	82.1	2610	2	AAZ21177	Aaz21177 Human AKT
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29	2099.5	82.1	2610	2	AAa09076	Aa09076 Wild type
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31	2099.5	82.1	2610	6	ABK84055	Abk84055 Human CDN
32	2099.5	82.1	2610	11	ADJ31880	Adj31880 Human CDN
33	2099.5	82.1	2610	12	ADL25354	Adl25354 Human ARK
34	2099.5	82.1	2610	12	ADP48782	Adp48782 Human Akt
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36	2004	78.3	1466	6	ABLS0838	Ab150838 Human Akt
37	2004	78.3	1593	12	ADQ84311	Adq84311 Human tum
38	2004	78.3	1593	13	ADQ86862	Adq86862 Human tum
39	2004	78.3	1593	13	ADQ83643	Adq83643 Human tum
40	2004	78.3	1593	13	ADQ85783	Adq85783 Human tum
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ALIGNMENTS

RESULT 1	AAA62451	standard; cDNA; 1440 BP.
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DT	13-NOV-2000	(first entry)
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DE	Human Akt-3 coding sequence.	
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KW	Human; Akt-3; protein kinase B; PKB; serine/threonine kinase; cytosolic;	
KM	apoptosis stimulator; cancer; rapid amplification of cDNA ends; RACE;	
KW	Chromosome 1q43-44; ss.	
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OS	Homo sapiens.	
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FH	Key	Location/Qualifiers
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FT		/product= "Akt-3"
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PN	WO200037613-A2.	
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PD	29-JUN-2000.	
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XX		
PF	17-DEC-1999;	99WO-GB004311.
XX		
PR	22-DEC-1998;	98GB-00028375.
XX		

PA (JANC) JANSSEN PHARM NV.

XX Masure SLJ, Richardson A;

XX WPI, 2000-498840/44.

DR P-PSDB; AAB13393.

XX New human serine/threonine kinase protein and the polynucleotide encoding
PT the protein, useful for preparing a medicament for treating disorders
PT associated with human serine/threonine kinase protein activity,
PT especially cancer.

PS Claim 4, Fig 1; 61np; English.

XX The present sequence is the coding region of the nucleotide sequence that
CC encodes human Akt-3. Akt-3 is a third human isoform of Akt, which is also
CC known as protein kinase B (PKB) or "related to A and C protein kinase"
CC (RAC-PK). The gene encoding Akt-3 is located on human chromosome 1,
CC region q43-q44. A human hippocampal EST sequence that showed high
CC similarity to the rat RAC-Pygamma sequence was used to design primers for
CC 3' rapid amplification of cDNA ends (3' RACE). The sequence obtained in
CC the first round of 3' RACE was used to design primers for a second round.
CC The complete sequence was then amplified from human hippocampal cDNA by
CC PCR using primers based on the product of the second round of 3' RACE.
CC Akt can inhibit apoptosis induced by detachment from the extracellular
CC matrix. The Akt-3 nucleic acid molecule and protein may be used as
CC medicaments for treating cancer. Agents which influence the activity of
CC Akt-3 protein, and so stimulate apoptosis, may also be used to treat
CC diseases associated with Akt-3

XX Sequence 1440 BP; 489 A; 248 C; 330 G; 373 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,18e-258 Length: 1440
Score: 2558.00 Matches: 479
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-869-079B-3 (1-479) x AAA62451 (1-1440)

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QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheserValAlaLysCysGln 60
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QY 81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTyrThrGlu 100
DB 241 ACTGTTATAGAGAACATTTTCATGTAGATCTCCAGAGAAAGGAGAAATGACAGAA 300
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DB 841 AAAGATGGCCACATAAATTTACAGATTTTGACCTTTCAGAAAGAGATCCACATGCA 900
QY 301 AlaThrMetLysThrPheCysGlyTyrProGluTyrLeuAlaProGluValLeuGluAsp 320
DB 901 GCCACCATGAAGACATTCGTGTGACCTCCAGAAATATCTGACAGAGGTTGTAAGAGAT 960
QY 321 AsnAspTyrGlyArgAlaValAspTyrProGlyLysLeuGlyValValMetTyrGluMetMet 340
DB 961 AATGACTATGGCCGAGAGATGACGTGTGGGCTTCAAGGAGTGTATGATGAATATGAG 1020
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGluLeuIleLeuMet 360
DB 1021 TGTGGAGGTTACCTTTCTACACACAGACCATGAGAACTTTTGAATATATTAATG 1080
QY 361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
DB 1081 GAAGACATTAATTTCTCTGAACACTCTCTTCAGATGCAAAATCATTTGCTTCAGGGCTC 1140
QY 381 LeuIleLysAspProAsnLysArgLeuGlyGlyTyrProAspAspAlaLysGluIleMet 400
DB 1141 TTGATTAAGAGATCCAAATTAAGCCTTGTGTGAGAGACAGATGATGCAGAAATATGAG 1200
QY 401 ArgHisSerPhePheSerGlyValAsnTyrGlnAspValTyrAspLysLeuValPro 420
DB 1201 AGACACAGTTTCTTCTCGAGTAACTGACAGATGATATATGATATAAAGCTTGACT 1260
QY 421 ProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
DB 1261 CTTTAAACCTCAAGTAAACATCTGACAGACATCTAGATATTTGATGAATAAATTTACA 1320
QY 441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCysMet 460
DB 1321 GCTCAGACTATTACATTAACACACCTGAAATAATGTAGAGAGATGTAGACGCAAG 1380
QY 461 AspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSerGlyValArgGlu 479
DB 1381 GACATGAGAGGCGCGCATTTCCCTCAATTTTCTACTCTGCAAGTGCAGAGAA 1437

RESULT 2
ABLS0839
ID ABL50839 standard; cDNA; 1440 BP.
AC ABL50839;
XX
DT 20-JUN-2002 (first entry)
XX

DE Human Akt3 encoding cDNA SEQ ID NO:10.
 XX
 XX Human; Hsp90 beta; Hsp90 alpha; Akt1; Akt2; Akt3; apoptosis regulation;
 KW apoptosis; serine/threonine kinase; heat shock protein; anticancer;
 KW cytoskeletal; cardiac; vasotrophic; hepatotrophic; neuroprotective;
 KW antidiabetic; neurotrophic; cancer; diabetes; Alzheimer's disease;
 KW cell death; radiation; brain ischaemia; cardiac ischaemia; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT CDS 1..1440
 FT /*tag= a
 FT /product= "Akt3"
 XX
 PN WO200215925-A1.
 PD 28-FEB-2002.
 PD 22-AUG-2001; 2001WO-JP007179.
 PF 22-AUG-2000; 2000JP-00251529.
 PR (TSUR/) TSURUO T.
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 PA (TSUR/) TSURUO T.
 PI Tsuruo T, Fujita N, Sato S;
 XX
 XX WPI; 2002-292035/33.
 DR P-PSDB; ABB06998.
 XX
 XX Regulation of apoptosis by promoting or inhibiting the intracellular
 PT binding of Akt with Hsp90, useful for prevention and treatment of
 PT apoptosis-regulation associated diseases including cancer.
 XX
 PS Disclosure; Page 87-89; 93pp; Japanese.
 XX
 CC The present invention describes the regulation of apoptosis, in which the
 CC intracellular binding of Akt (a serine/threonine kinase) with Hsp90 (a
 CC heat-shock protein) is promoted or inhibited. The present invention also
 CC describes: (1) isoforms of Akt and Hsp90, and their partial peptides
 CC including the binding domain; (2) antibodies to Akt or Hsp90; (3) DNA
 CC encoding Akt or Hsp90 or their partial peptides including the binding
 CC domain; (4) expression vectors containing the DNA; (5) host cells
 CC transformed by the vectors; (6) production of Akt or Hsp90 or their
 CC partial peptides including the binding domain by culture of the
 CC transformed cells; (7) screening compounds for their ability to modify
 CC intracellular Akt activity by contact with cells expressing Akt or Hsp90;
 CC and (8) drug compositions containing antibodies recognizing the binding
 CC domain of Akt or Hsp90 and optionally also an anticancer agent. Akt and
 CC Hsp90 have cytoskeletal, cardiac, vasotrophic, hepatotrophic, antidiabetic,
 CC neuroprotective and neurotrophic activities. Blockade of the binding of
 CC Hsp90 with Akt increases the sensitivity of cells to apoptosis induction.
 CC Akt and Hsp90 can be used in the prevention and treatment of diseases
 CC with which apoptosis regulation is associated, including cancer (such as
 CC gastric cancer, ovarian cancer, breast cancer, pancreatic cancer and
 CC prostate cancer), diabetes, Alzheimer's disease, cell death caused by
 CC radiation or anticancer agents, brain ischaemia or cardiac ischaemia. The
 CC present sequence encodes human Akt3 which is used in the exemplification
 CC of the present invention
 XX
 SO Sequence 1440 BP; 489 A; 248 C; 330 G; 373 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.18e-258 Length: 1440
 Score: 2558.00 Matches: 479
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-869-079B-3 (1-479) x ABL50839 (1-1440)

QY 1 MetSerAspValThrIleValIleGluGluYTPValGlnLysArgLysGluYrIleLys 20
 DB 1 ATGAGCGATGTTACATCTGTGAAAGAGGTGGGTTCAAGAGCGGAGAAATTATATAAA 60
 QY 21 AsnTrpArgProArgTrpPheLeuLeuLysTrpAspGlySerPheIleGlyYrIleGlu 40
 DB 61 AACTGAGGCGCAAGATACCTTCCTTTGAAAGACAGATGGCTCATTTACATAGATATAAAG 120
 QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheSerValAlaLysCysGln 60
 DB 121 AAACCTCAAGATGTGATTTACCTTATCCCTCAACACTTTTCATGTGGCAAAATCCAG 180
 QY 61 LeuMetLysThrGlnArgProLysProAsnThrPheIleIleArgCysLeuGlnTyrTrp 80
 DB 181 TTATATGAACAGAACAGACCAAGCCAAACATTTATATACATGATGTCTCCAGTGGACT 240
 QY 81 ThrValIleGluArgTrpPheHisValAspThrProGluGluArgGluGluYrTrpTrgln 100
 DB 241 ACTGTTATAGAGAAACATTTCACTGATGATCTCCAGAGAAAGGAAATGACAGAA 300
 QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetLysCysSer 120
 DB 301 GCTATCCAGGCTGTAGCAGACACTGCAGAGCAAGAGAGAGAGAAATGAAATTTAGT 360
 QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrTrpHis 140
 DB 361 CCAACTTCACAAATGTATATATAGAGAGAAAGATGATGCTCTCAACCCATCAT 420
 QY 141 LysArgLysThrMetAsnAspPheAspTrpLeuLysLeuLysGlyYrPheGlyYrPheGly 160
 DB 421 AAAGAAACACATGATGATTTTGACTATTTGAAACTAGTAAAGGACCTTTGGG 480
 QY 161 LysValIleLeuValArgGluLysLysAspGlyYrYrTrpAlaMetLysIleLeuLys 180
 DB 481 AAAGTATTTGGTTCGAGAGAGGCAAGTGAATAATCTATGCTGTGAAGATTCGGAAG 540
 QY 181 LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArgValIle 200
 DB 541 AAAGAAAGCATTTATGCAAGAGTGAAGTGGCACACACTCTAACTGAAGCAGATATTA 600
 QY 201 LysAsnThrArgHisAspPheLeuThrSerLeuLysYrYrSerPheGlnThrLysAspArg 220
 DB 601 AAGAACACATGACATCCCTTTTAAACATCTTGAATATTCCTTCAGACAAAGACCGT 660
 QY 221 LeuCysPheValMetGluYrValAsnGlyGlyGluLeuPhePheHisLeuSerArgGlu 240
 DB 661 TTGTGTTTGTGATGGAATATGATGGGGGAGCTGTCTTTTCCATTTGTTCGAAAGAG 720
 QY 241 ArgValPheSerGluAspArgThrArgPheYrGlyValGlnIleValSerAlaLeuAsp 260
 DB 721 CGGGTGTCTCTGAGGACCGCACAGCTTCTATGTGCGAAGAAATGTCTCTGCTTGAC 780
 QY 261 TyrLeuHisSerGlyLysIleValIYrArgAspLeuLysLeuGlnAsnLeuMetLeuAsp 280
 DB 781 TATCTACATCTCGGAAAGATGTGTACCTGATCTCAATTTGAGAAATCTTAATGCTGGAC 840
 QY 281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIleThrAspAla 300
 DB 841 AAAAGATGCCACATAAATAATTCAGATTTTGACCTTGCAGAAAGAGGATCAAGATGCA 900
 QY 301 AlaThrMetLysThrPheCysGlyThrProGluYrYrLeuAlaProGluValLeuGluAsp 320
 DB 901 GCCACCATTAAGACATCTGTGGCACTCCAGAAATATCTGCACACAGAGGTGTAGAGAGT 960
 QY 321 AsnAspTrpGlyYrArgAlaValAspTrpTrpGlyLysGluValValMetYrGluMetCys 340
 DB 961 AATGATTAATGCGCGGACATTAAGTCTGTGGGCTTGAAGGTTGTATGATGAATGAATG 1020
 QY 341 CysGlyYrArgLeuProPheYrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
 DB 1021 TGTGGAGAGGTTACCTTTCTACAAACGACGACATGAGAAATCTTTGAATTAATTAATG 1080
 QY 361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380

DB 1081 GAAGACATTAATTTCTCGAACACTCTCTTGATGCAAAATCATTTGCTTCAGGGCTC 1140
 QY 381 Leu111eLysAspProAsnLysArgLeuGlyGlyGlyProAspAspAlaLysGluMet 400
 DB 1141 TGGATTAAGAGATCAATATAACCCCTTGGGAGGACCAAGTATCAAAAGAAATTAAG 1200
 QY 401 ArgHisSerPhePheSerGlyValAsnTPGAlaSerValTyrAspLysLysLeuValPro 420
 DB 1201 AGACACAGTTTCTTCTCTGAGTAACCTGGCAAGATGTATATGATATAAAAGCTTGACT 1260
 QY 421 ProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGluLuphetr 440
 DB 1261 CCTTTAAACCTCAAGTAACTGAGACAGATACTAGATATTGATGAGAAATTACA 1320
 QY 441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCysMet 460
 DB 1321 GCTCAACACTATTAACAATAACACCACTGAAAAATATGATGAGATGTATGACTGCAATG 1380
 QY 461 AspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSerGlyArgGlu 479
 DB 1381 GACAAATGAGAGCGCGCCGATTTCTCTCAATTTTCTTACTCTGCAAGTGAGAGAGA 1437

RESULT 3.

AAA62450
 ID AAA62450 standard; cDNA; 1547 BP.

XX AAA62450;

DT 13-NOV-2000 (first entry)

DE Human Akt-3 nucleotide sequence.

KM Human: Akt-3; protein kinase B; PKB: serine/threonine kinase; cytosolic;
 apoptosis stimulator; cancer; rapid amplification of cDNA ends; RACE;
 chromosome 1q43-44; 8s.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 11..1450

FT /tag= a

FT /product= "Akt-3"

FT /note= "nucleotides 11 to 1447 are given as SEQ ID NO: 2

FT in the specification and are specifically claimed in

FT claim 4 (see AAA62451)"

XX WO200037613-A2.

XX 29-JUN-2000.

XX 17-DEC-1999; 99WO-GB004311.

XX 22-DEC-1998; 98GB-00028375.

XX (JANNC) JANSEN PHARM NV.

XX Masure SLJ, Richardson A;

XX WPI, 2000-498840/44.

XX P-PSDB; AAB13393.

XX New human serine/threonine kinase protein and the polynucleotide encoding

XX the protein, useful for preparing a medicament for treating disorders

XX associated with human serine/threonine kinase protein activity,

XX especially cancer.

XX Claim 3; Fig 1; 61pp; English.

XX The present sequence encodes human Akt-3. Akt-3 is a third human isoform

XX of Akt, which is also known as protein kinase B (PKB) or "related to A

XX and C protein kinase" (RAC-PK). The gene encoding Akt-3 is located on

XX human chromosome 1, region q43-q44. A human hippocampal EST sequence that

CC showed high similarity to the rat RAC-PKgamma sequence was used to design
 CC primers for 3' rapid amplification of cDNA ends (3' RACE). The sequence
 CC obtained in the first round of 3' RACE was used to design primers for a
 CC second round. The complete sequence was then amplified from human
 CC hippocampal cDNA by PCR using primers based on the product of the second
 CC round of 3' RACE. Akt can inhibit apoptosis induced by detachment from
 CC the extracellular matrix. The Akt-3 nucleic acid molecule and protein may
 CC be used as medicaments for treating cancer. Agents which influence the
 CC activity of Akt-3 protein, and so stimulate apoptosis, may also be used
 CC to treat diseases associated with Akt-3

XX SQ Sequence 1547 BP; 515 A; 276 C; 348 G; 408 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1..3e-258	Length:	1547
Score:	2558.00	Matches:	479
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-09-869-079B-3 (1-479) x AAA62450 (1-1547)

QY 1 MetSerAspValThrIleValIysGluGlyTyrValGlnLysArgGlyGluTyrIleLys 20

DB 11 ARGAGGATGTATACCATGTGTGAAGAAGGTGGTTGAGAAAGGGGAGAAATATATAAA 70

QY 21 AsnTPArgProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrIysGlu 40

DB 71 AACTGAGGCCAAGATCTCTCTTTGAAGACAGATGGCTCATTTATGAGATATAAGG 130

QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheSerValAlaLysCysGln 60

DB 131 AAACCTCAAGATGTGATTTACTTATCCCTCAACAACCTTTGATGGCAAAATGCCAG 190

QY 61 LeuMetLysThrGluArgProLysProAsnThrPheIleLysCysLeuGlnTyrThr 80

DB 191 TTAATGAANAACAGAACGACCAAGCAACCAATTTATATCATGATGCTCCAGTGACT 250

QY 81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGlnTyrThrGlu 100

DB 251 ACTGTTATAGAGAAACATTTGATGATGATCTCCAGAGAAAGGAGAAATGACACAGA 310

QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCysSer 120

DB 311 GCTATCCAGCTGTGACGACGACTGACAGGCAAGAGAGAGATGATGATTTGACT 370

QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSerThrThrHis 140

DB 371 CCAACTTCACAATTTGATATATAGAGAGGAAAGATGATGCTCTTACCAACCATCAT 430

QY 141 LysArgLysThrMetAspAspPheAspTyrLeuLysLeuLysGlyLysThrPheGly 160

DB 431 AAAGAAAGACATGATATGATTTTGAATCTATGAGTAAGGACCTTTGGG 490

QY 161 LysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAlaMetLysIleLeuLys 180

DB 491 AAAGTTATTTTGCTTCGAGAGAGGCAAGGCAAAATCTATGCTATGAGATTCGAAAG 550

QY 181 LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArgValLeu 200

DB 551 AAAGAAAGTCAATTAATGCAAGATGAGAGGACACACTCTAAGAAAGCAGAGATTA 610

QY 201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220

DB 611 AAGAACACTAGACATCCCTTTTAACTCTTGAATATCTCTTCAGCAAAAGACGT 670

QY 221 LeuCysPheValMetGluTyrValAsnGlyGlyLysLeuPheHisLeuSerArgGlu 240

DB 671 TTGTGTTTGTGATGGAATATCTTAATGGGGCGAGCTCTTTTTCATTGTTCGAGAGG 730

QY 241 ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGlnIleValSerAlaLeuAsp 260

Db 731 CGGGTGTCTCTGAGAGACCGACACGTTTCTATGTGTCAGAAAATTGTCCTGCGCTTGAC 790
 Qy 261 TTTLeuHiseSerGlyLysIleValIYrAAspLeuLysLeuGluAAsnLeuMetLeuAsp 280
 Db 791 TATCTACATTCGCGAAAGATTGTGTACCTGATCTCAAGTTGAGAACTTAAGCTGAC 850
 Qy 281 LysAspGlyLysIleLysIleThrAspPheGlyLeuLysLysGluGlyIleThrAspAla 300
 Db 851 AAAGATGGCCACATTAATAATTCAGATTGTGACTTTGGCAAGAGAGGATCCACAGATGCA 910
 Qy 301 AlaThrMetLysThrPhePheCysGlyLysThrProGluLysLeuAlaProGluValLeuGluAsp 320
 Db 911 GCCACCATGAAAGACATTCCTGTGACATCCAGAAATATCTGSCACACAGAGGCTTGAAGAT 970
 Qy 321 AsnAspTYrGlyLysGalaValAspTYrTYrGlyLysLeuGlyValValMetTYrGluMetMet 340
 Db 971 AATGACTATGCGCAGACAGATGACTGGTGGGGCTGAGGGGTTGTCATGATGTGAAGATGATG 1030
 Qy 341 CysGlyAryGleuProPheTYrAsnGlnAspHisGluLysLeuPheGluLeuMetMet 360
 Db 1031 TGTGGAGGTTACCTTCTACACACAGACCATGAGAACTTTTGAAATTAATTAATGATG 1090
 Qy 361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
 Db 1091 GAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTGCTTTCAGGGCTC 1150
 Qy 381 LeuIleLysAspProAsnLysValGleuGlyGlyGlyProAspAspAlaLysGluIleMet 400
 Db 1151 TTGATTAAGATCCAAATAAACCCCTTGCTGGAGGACCAAGATATGCAAAAGAAATATG 1210
 Qy 401 ArgHisSerPhePheSerGlyValAsnTYrGlnAspValTYrAspLysLysLeuValPro 420
 Db 1211 AGACACAGTTTCTCTGTGAGTAAGTGGCAAGATTAATGATTAATAAAAGCTTGATCCT 1270
 Qy 421 ProPheLysProGluValThrSerGluThrAspThrArgTYrPheAspGluGluPheThr 440
 Db 1271 CTTTTAAACCTCAAGTAACATCTGAGACAGATGATGATTTTGTATGAAGATTTACA 1330
 Qy 441 AlaGlnThrIleThrIleThrProProGluLysTYrAspGluLysGluMetAspCysMet 460
 Db 1331 GCTCAGACTATTAACAATAACACACCACTGAAGAAATATGATGAGATGCTGATGCACTGCATG 1390
 Qy 461 AspAspGluAryArgProHisPheProGlnPheSerTYrSerAlaSerGlyAryGlu 479
 Db 1391 GACAAATGAGAGGCGCGCATTTCCCTCAATTTTCTACTCTGCAAGTGGACGAGAA 1447
 RESULT 4
 ADN71939
 ID ADN71939 standard; cDNA; 1547 BP.
 AC ADN71939;
 DT 12-AUG-2004 (first entry)
 XX Human serine/threonine kinase Akt-3 encoding cDNA SEQ ID NO:25.
 DE
 KW kinase pathway inhibitor; anti-prostate cancer;
 KW mitogen-activated protein kinase pathway inhibitor;
 KW MAP kinase pathway inhibitor; prostate cancer inhibitor;
 KW phosphatidylinositol 3-kinase/Akt kinase pathway;
 KW PI3K/Akt kinase pathway; cytoskeletal MAP kinase inhibitor;
 KW phosphatidylinositol 3-kinase/Akt kinase inhibitor;
 KW PI3K/Akt kinase inhibitor; androgen receptor inhibitor; prostate cancer;
 KW human; serine/threonine kinase Akt-3; chromosome 1; gene; ss.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 11..1450
 FT /*tag= a
 FT product= "serine/threonine kinase Akt-3"
 XX
 PN MO2004041185-A2.

XX
 PD 21-MAY-2004.
 XX
 PF 31-OCT-2003; 2003WO-US034636.
 XX
 PR 31-OCT-2002; 2002US-0423340P.
 XX
 PA (UYRP) UNIV ROCHESTER.
 XX
 PI Chang C, Lee Y, Lin W;
 XX
 DR WPI; 2004-390508/36.
 DR P-PSDB; ADN71940.
 XX
 PT Composition useful in the treatment of e.g. prostate cancer comprises a
 PY kinase pathway inhibitor and an anti-prostate cancer compound.
 PS
 PS Disclosure; SEQ ID NO 25; 118pp; English.
 CC The present invention describes a composition (C1) which comprises a
 CC kinase pathway inhibitor (a) and an anti-prostate cancer compound (b).
 CC Also described: (1) identification of a mitogen-activated protein (MAP)
 CC kinase pathway inhibitor involving incubating an androgen or a
 CC library of molecules with a cell containing an activable MAP kinase
 CC pathway and selecting the molecules which inhibit the activation of the
 CC MAP kinase pathway; and (2) identification of a prostate cancer inhibitor
 CC involving incubating a cell with hydroxylutamide and potential
 CC inhibitor, and assaying the level of activation of MAP kinase pathway or
 CC phosphatidylinositol 3-kinase (PI3K)/Akt kinase pathway. C1 has
 CC cytostatic activity, and can be used as a MAP kinase inhibitor,
 CC phosphatidylinositol 3-kinase (PI3K)/Akt kinase inhibitor, and androgen
 CC receptor (AR) inhibitor. C1 can be used in the treatment of prostate
 CC cancer; for identifying a MAP kinase pathway inhibitor; for identifying a
 CC prostate cancer inhibitor; and for reducing the number of prostate cancer
 CC cells in a sample. The composition C1 provides effective combination
 CC therapy as compared to prior therapies. The present sequence encodes
 CC human serine/threonine kinase Akt-3, which is used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 1547 BP; 515 A; 276 C; 348 G; 408 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 1,3e-258 Length: 1547
 Score: 2558.00 Matches: 479
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0
 US-09-869-079B-3 (1-479) x ADN71939 (1-1547)
 Qy 1 MetSerAspValThrIleValLysGluGlyTYrTPValGlnLysArgGlyLysIleLys 20
 Db 11 ATGAGCGAGTTRACATTTGTGAAGAAGGTGGGTTCAAGAAGGGGAGAAATATATATAAA 70
 Qy 21 AsnTPArgProArgTYrPheLeuLeuLysIleThrAspGlySerPheIleGlyTYrLysGlu 40
 Db 71 AACTGAGGCGCAAGAAATCTCTTTTGAAGACAGAGGCTCATCTTACATGATTAATAAGAG 130
 Qy 41 LysProGluAspValAspLeuProTYrProLeuAsnAspPheSerValAlaLysCysGln 60
 Db 131 AAACCTCAAGATGGATTTTACCTTATCCCTCAACAACCTTTTCAATGGCAAAATGCCAG 190
 Qy 61 LeuMetLysThrGluAryArgProLysProAsnThrPheIleIleArgCysLeuGlnTYrThr 80
 Db 191 TTATGAAAAACGAAGACCAAAAGCAAAACATTTATATATGATGATGTCTCCAGTGACT 250
 Qy 81 ThrValIleGluAryThrPheHisValAspThrProGluGluLysGluLysIleLysGlu 100
 Db 251 ACTGTTATGAGAGAACTTTCAATGATGATCTCCAGAGAAAGGAGAAATGAGACAGAA 310
 Qy 101 AlaIleGluAlaValAlaAspArgLeuGlnArgGluGluGluLysGluMetAspCysSer 120

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Db      311 GCTATCCAGGCTGTACAGACAGACTGCAGAGCCAAAGAGAGAGAAATGATTGTAGT 370
Qy      121 ProThrSerGlnIleAspAsnIleGluGluMetAspAlaSerThrHis 140
Db      371 CCACTTCACAAATATATATAGAGAGAGAGATGATGCTCTCAACACCACTCAT 430
Qy      141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuLysGlyThrPheGly 160
Db      431 AAAAGAAAACATGATGATGATTTGACTATTGAAACCTAGTAAAGCACTTTGGG 490
Qy      161 LysValIleLeuValAlaArgLysValAspGlyLysTyrTyrAlaMetLysIleLeuLys 180
Db      491 AAAGTATATTTGGTTGAGAGAGAGAGAGAAATGACTATGCTTGAAGATTCGAAG 550
Qy      181 LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArgValLeu 200
Db      551 AAAAGAGTCATTTTCCAAAGATGAGAGTGGCACACACTCTAACTGAAAGCAGATTTTA 610
Qy      201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
Db      611 AAGAACACTAGACATCCCTTTTAAACATCCTTGAAATATTCCTCCAGCAAAAGACCGT 670
Qy      221 LeuCySPheValMetGluTyrValaAsnGlyGlyGluLeuPhePheHisLeuSerArgGlu 240
Db      671 TTGTGTTTTGTGTGATGAAATATGTTAATGGGGGCGACCTGTTTTCCATTGTCGAGAGAG 730
Qy      241 ArgValPheSerGluAspArgThrArgPheTyrGluAlaGluIleValSerAlaLeuAsp 260
Db      731 CCGGTGTTCTTGAGAGACCGCACACGTTCTATGTCGAAATTTGCTCTGCTTGGAC 790
Qy      261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
Db      791 TATCTACATTCGCGAAAGATTTGTGTACCGTGATCTCAAGTTGAGAAATCAATAGCTGGAC 850
Qy      281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCySPheGlyGluGlyIleThrAspAla 300
Db      851 AAAGATGGCCACATTAATAATTCAGATTTTGACCTTTGCAAAAGAGATCAACAGATGCA 910
Qy      301 AlaThrMetLeuThrPheCySPheGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
Db      911 GCCACCATTAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCAAGGTGTTAGAAAGT 970
Qy      321 AsnAspTyrGlyArgAlaValAspTyrPheGlyLeuGlyValaMetTyrGluMetMet 340
Db      971 AATGACTATGCGCGACAGACAGACTGTGTGGGCGCTGAGGGGTGTATGATGAATGATG 1030
Qy      341 CySPheArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
Db      1031 TGTGGAGAGGTACCTTTCTTACACACGACCATGAGAAAACCTTTTGAATTAATTAAATG 1090
Qy      361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
Db      1091 GAAAGACATTAATTTCTCGAACACTCTCTTCGATGCAAAATCATGCTTTTCAGGGGCTC 1150
Qy      381 LeuIleLysAspProAsnLysArgLeuGlyGlyIleProAspAspAlaLysGluIleMet 400
Db      1151 TTGATTAAGAGATCCAATATAACCGCTTGTGGAGGACCAAGATGATCAAAAGAAATTATG 1210
Qy      401 ArgHisSerPhePheSerGlyValaAsnTyrPheGluAspValTyrAspLysLeuValPro 420
Db      1211 AAGACACAGTTTTCTCTCTGAGTAACTGGCAGAGATGATATGATTAATAAGCTTGTACCT 1270
Qy      421 ProPheLysProGluValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
Db      1271 CCTTTAAACCTCAATATACATCTGAGACAGATACATGATATTTGATGAAAGATTTTAA 1330
Qy      441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCySPhe 460
Db      1331 GCTCAGACTATTAACAATAACACCACTGAAAAATATGATGAGAGATGATGATGATGATG 1390
Qy      461 AspAsnGluArgArgProHisPhePheProGluPheSerLysSerAlaSerGlyArgGlu 479
Db      1391 GACAAATGAGAGGGGCGGCAATTTCCCTCAATTTTCTACTCTGCAAGTGGAGAGAA 1447

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RESULT 5
AAC61592
ID AAC61592 standard, DNA; 2367 BP.
XX
AC AAC61592;
XX
DT 19-FEB-2001 (first entry)
XX
DE DNA encoding a human kinase B-gamma polypeptide.
XX
XX Human; protein kinase B gamma; PKB; insulin; insulin growth factor 1;
XX phosphoinositide 3-kinase; insulin signalling;
XX pleckstrin homology domain; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 10..1449
FT /tag=a
FT /product="kinase B-gamma polypeptide"
XX
XX MO200058446-A1.
XX
XX 05-OCT-2000.
XX
XX 23-MAR-2000; 2000MO-SE000571.
XX
XX 25-MAR-1999; 99SE-00001115.
XX
XX (PHMA ) PHARMACIA & UPJOHN AB.
XX
XX Altersand A;
XX
XX WPI; 2000-647230/62.
XX
XX P-PSDB; AAB19284.
XX
XX
XX Novel human protein kinase B gamma polynucleotides and polypeptides
XX useful as probe or primers in polymerase chain reaction and to raise
XX antibodies useful in diagnostic assays for detecting polypeptide
XX expression.
XX
XX Claim 1; Page 16-19; 27pp; English.
XX
XX
XX The present sequence encodes a human protein kinase B gamma (PKB)
XX polypeptide. PKB is activated by insulin or insulin growth factor 1.
XX Lipid products of phosphoinositide 3-kinase act in insulin signalling by
XX binding to pleckstrin homology domains of PKB. PKB polynucleotides may be
XX used as a source of probes and primers. PKB polypeptides are used to
XX raise antibodies, which are used in diagnostic assays. The polypeptides
XX are also useful for screening for compounds which affect insulin
XX signalling pathways
XX
XX Sequence 2367 BP; 752 A; 444 C; 514 G; 657 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 2,326-258 Length: 2367
XX Score: 2558.00 Matches: 479
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 3 Gaps: 0
XX
XX
XX US-09-869-079B-3 (1-479) x AAC61592 (1-2367)
XX
XX
XX 1 MetSerAspValThrIleValLysGluGlyTyrPValGluLysArgGlyGluTyrIleLys 20
XX 10 ATGAGCGAGATGTACCATTTGTGAAGAAGGTTGCTCAGAAAGGAGAGAAATATATAAAA 69
XX
XX 21 AsnTPArgProArgTyrThrLeuLeuLysThrAspGlySerPheIleGlyTyrTyrGlu 40
XX 70 AACTGAGAGCCAAAGTACTTCTTTTGAAGACAGATGGCTCATTCATGAGATATAAAG 129

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QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAspPheSerValAlaLysCysGln 60
 DB 130 AAACCTCAAGATGGATTTTACTTATCCCTCAACACTTTTCACTGGCGAAATGCGAC 189
 QY 61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTrpThr 80
 DB 190 TTAATGAAACAGAACGACCAAGCAACCAACATTTATATATCATGATGTCCTCGATGACT 249
 QY 81 ThrValIleGluLysArgThrPheHisValAspThrProGluGluLysGluLysTrpGlu 100
 DB 250 ACTGTTATAGAGAACATTTCATGTAGATATCCAGAGAAAGGAAAGATAGACAGAA 309
 QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGluGluGluLysTrpMetAsnCysSer 120
 DB 310 GCTATCAGGCTGTAGACAGACACTGCGAGAGCGAGAGAGAGAGATGAAATTTGTAAT 369
 QY 121 ProThrSerGlnIleAspAsnIleGluGluGluMetAspLysSerThrTrpHis 140
 DB 370 CCMACTTCAAAATTTGATATATATAGAGAGAGAGATGATGCTCTACACCATCAT 429
 QY 141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGluLysGluLysTrpPheGly 160
 DB 430 AAAAGAAAGCAATGATGATTTTGAATTTGAACTACTAGTAAAGGCACCTTTGGG 489
 QY 161 LysValIleLeuValArgGluLysValAspSerGluLysTyrTrpAlaMetLysIleLeuLys 180
 DB 490 AAGATTATTTTGTGAG 549
 QY 181 LysGluValIleIleIleLysAspGluValAlaHisThrLeuThrGluSerArgValLeu 200
 DB 550 AAAGAAGTCATTATTCGAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATTA 609
 QY 201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
 DB 610 AAGAACACTAGACATCCCTTTTAAACATCCCTGAAATATCTTCCAGCAAAAGACCGT 669
 QY 221 LeuCysPheValMetGluTyrValAlaAsnGluGluLeuPhePheHisLeuSerArgGlu 240
 DB 670 TTGTGTTTGTGATGAGAAATGTTAAATGGGGGCGAGCTGTTTCCATTTGTGAGAGAG 729
 QY 241 ArgValPheSerGluAspArgThrArgPheTyrGluValGluLysIleValSerAlaLeuAsp 260
 DB 730 CCGGTGTTCTCTGAG 789
 QY 261 TyrLeuHisSerGluLysIleValIlyrArgAspLeuLysLeuGluLysLeuMetLeuAsp 280
 DB 790 TATCTCATTTCCGGAAGATTTGTGTACCGTGAATCTCAAGTTGAGAGATCTAAATGCTGAG 849
 QY 281 LysAspGluHisIleLysIleThrAspPheGluLysCysLeuGluGluLysIleThrAspAla 300
 DB 850 AAAGATGGCCACATAAATTTACAGATTTTGGACTTTGCAAAAGAGAGATCACAGATGCA 909
 QY 301 AlaThrMetLysThrPheCysGluLysTrpGluLysLeuLysLeuLysLeuLysLeuLys 320
 DB 910 GCCACATGAGACATTTCTGTGCACTCCAGATATCTGSCACAGAGGTGTTAAGAAAT 969
 QY 321 AsnAspTyrGluArgAlaValAspTrpTrpGluLysGluValValMetTyrGluMetMet 340
 DB 970 AATGACTATGCGCGACAGACAGTGTGTGGGCTGAGGCTGTCTCATGTATGAAATGATG 1029
 QY 341 CysGluArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuLysMet 360
 DB 1030 TGTGGGAGGTACCTTTCTACAAACGAGACCAATGAAATTTTAAATTAATTAATTAAT 1089
 QY 361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGluLys 380
 DB 1090 GAAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTTCTTCAAGGCTC 1149
 QY 381 LeuIleLysAspProAsnLysArgLeuGluGluLysGluLysProAspAspAlaLysGluIleMet 400
 DB 1150 TTGATTAAGAGATCAATTAATTAACCCCTTGTGTGAGAGACAGATGATCAAAAGAAATTAAT 1209
 QY 401 ArgHisSerPhePheSerGluValAsnTrpGlnAspValTyrArgLysLysLeuValPro 420

DB 1210 AGCACAGATTTCTTCTCTGAGATGAACCTGCAAGATGATATATATAAAAGCTTACTAC 1269
 QY 421 ProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
 DB 1270 CTTTAAACCTCAACTAATCATCTGAGACAGATATATTTGATGAGAAATTTTACA 1329
 QY 441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGluMetAspCysMet 460
 DB 1330 GCTCAACATTAATTAACATTAACCTGAAATATGATGATGATGATGATGATGATG 1389
 QY 461 AspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSerGluArgGlu 479
 DB 1390 GACAAATGAGAGCGCGCCGATTTCCCTCAATTTTCTTACTCTGCAAGTGCAGAGAA 1446
 RESULT 6
 ADCC26888 standard; DNA; 2811 BP.
 ID ADCC26888
 AC ADCC26888:
 XX 18-DEC-2003 (first entry)
 DT 18-DEC-2003 (first entry)
 XX 18-DEC-2003 (first entry)
 DE DNA encoding human Akt3.
 KW de; gene; Akt; human; apoptosis; myocardial infarction;
 KW hyperproliferative disease; cancer; rheumatoid arthritis;
 KW inflammatory bowel disease; osteoarthritis; leiomyoma; adenoma;
 KW haemangioma; fibroma; vascular occlusion; restenosis; atherosclerosis;
 KW pre-neoplastic lesion; adenomatous hyperplasia;
 KW prostatic intraepithelial neoplasia; carcinoma in situ;
 KW oral hairy leukoplakia; psoriasis.
 KW
 OS Homo sapiens.
 OS
 PN US2003144204-A1.
 XX
 PD 31-UTL-2003.
 XX
 PF 19-DEC-2002; 2002US-00324985.
 XX
 PR 19-DEC-2001; 2001US-0342155P.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Spencer D;
 XX
 DR WPI; 2003-720709/68.
 XX
 PT New expression vector for modulating apoptosis or for treating myocardial
 PT infarction or cancer, comprises an inducible chimeric protein that
 PT comprises a mutant Akt polypeptide fused to a ligand-binding domain.
 PS Disclosure; SEQ ID NO 4; 38pp; English.
 PS
 CC The invention relates to an expression vector comprising an inducible
 CC chimeric protein which comprises a mutant Akt polypeptide fused to a
 CC ligand-binding domain. The composition and methods are useful in
 CC modulating apoptosis or in treating myocardial infarction or
 CC hyperproliferative diseases such as cancer, rheumatoid arthritis,
 CC inflammatory bowel disease, osteoarthritis, leiomyoma, adenoma,
 CC lipoma, haemangioma, fibroma, vascular occlusion, restenosis,
 CC atherosclerosis, pre-neoplastic lesions (e.g. adenomatous hyperplasia or
 CC prostatic intraepithelial neoplasia), carcinoma in situ, oral hairy
 CC leukoplakia or psoriasis. The present sequence represents DNA encoding
 CC human Akt3.
 CC
 SQ Sequence 2811 BP; 905 A; 506 C; 582 G; 818 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2,93e-258 Length: 2811
 Score: 2558.00 Matches: 479
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-869-079B-3 (1-479) x ADC26888 (1-2811)

QY 1 MetSerAspValThrIleValLysGluGlyTTPValGlnLysArgGlyLysTyrIleLys 20
DB 1 ATGAGGAGTGTATCCATTGTGAAGAAGGTGGGTTCAAGAGGGGGAATATATATAA 60
QY 21 AsnTPArgProArgTyrPheLeuLeuLysTyrAspGlySerPheIleGlyTyrLysGlu 40
DB 61 AACTGAGGCGCAAGATACCTCTTCTTGAAGACAGATGGCTCATCTTCAAGATATATAAG 120
QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheSerValAlaLysCysGln 60
DB 121 AAACCTCAAGATGGAGATTTACCTTATCCCTTCAACACTTTTCACTGGCAAAATCCAG 180
QY 61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTTPThr 80
DB 181 TTATGATAAACAAGACGACCAAGCAACATTTATATCATGATGCTCCAGTGAAGT 240
QY 81 ThrValIleGluArgThrPheIleValAspThrProGluGluArgGluLysTTPThrGlu 100
DB 241 ACTGTTATAGAGAACATTTTCATGTAGTACTCCAGAGAAAGGAAAGATGACAGAA 300
QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCysSer 120
DB 301 GCTATCAAGCTGTACAGACAGACTGCAGAGGCAAGAGAGAGAAATGAAATTTAGT 360
QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSerThrThrHis 140
DB 361 CCACACTTCACAATTTATATATATAGAGAGAGAAAGATGATGCTCTCAACACCATCAT 420
QY 141 LysArgLysThrMetLysAspPheAspTyrLysLysLeuLeuGlyLysGlyTyrPheGly 160
DB 421 AAAAGAAACACATGATGATGATTTTGACTATTTGAAACTATGATAAGCACTTTTGGG 480
QY 161 LysValIleLeuValArgLysLysAspSerGlyLysTyrTyrAlaMetLysIleLeuLys 180
DB 481 AAGATTATTTGGTTGAGAGAGAGCAAGTGGAAATACATAGCTTATGAAATTTCTGAAG 540
QY 181 LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGlnSerArgValLeu 200
DB 541 AAAGAGTCATATATTCAAAGATGAGTGAAGTGGCACACACTCACTAAAGCAGAGATTA 600
QY 201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
DB 601 AAGAACACATAGACATCCCTTTTAAACATCTTGAAATATTTCCCTTCCAGCAAAAGACGT 660
QY 221 LeuCysPheValMetGluTyrValLaengLysGlyLeuPhePheHisLeuSerArgGlu 240
DB 661 TTGGTTTGTGTATGGAAATATGTTAATGGGGGCGACCTGTTTTTCCATTTGTTCGAGAG 720
QY 241 ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAlaLeuAsp 260
DB 721 CGGGTGTCTCTGAGGACCGCACACGTTCTATGAGCAAAATGTCTCTGCTTGAGAC 780
QY 261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGlnAsnLeuMetLeuAsp 280
DB 781 TATCTACATTTCCGAAAGATTTGTATCCGATCTAAGTTGGAGAAATCTAAAGCTGAGAC 840
QY 281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCysLeuGluGlyIleThrAspAla 300
DB 841 AAAAGATGGCCACATAAAATTTACAGATTTTGAATTTGCCAAAGAGAGGATCACAGATGCA 900
QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
DB 901 GCCACATAGAGCAATTTCTGTGCACTCCAGAAATATCTGGCACCAAGGTTTAAAGAAAT 960
QY 321 AsnAspTyrGlyArgAlaValAspTyrTTPGlyLysGlyValAlaMetTyrGluMetMet 340
DB 961 AATGACTATGGCGAGACAGTAGACTGTGTGGGCTTGGGGTGTGTATGTAATAATGATG 1020

QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
DB 1021 TGTGGAGGATTAACCTTTCTTCAACAACGAGACCATGAAACTTTTGAATATATATTAATG 1080
QY 361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
DB 1081 GAAGACATTAATTTCTCTGAAACACTCTTCTCAGATGCAAAATCATTTGCTTTCAGGGCTC 1140
QY 381 LeuIleLysAspProAsnLysArgLeuGlyGlyGlyProAspAspAlaLysGluIleMet 400
DB 1141 TTGATTAAGATCCAAATTAACGCTTGTGTGAGAGCCAGAGATGACAAATAATTTATG 1200
QY 401 ArgHisSerPhePheSerGlyValAsnTPGlnAspValTyrAspLysLeuValPro 420
DB 1201 AGACACAGTTTCTTCTGAGATTAACGCAAGATGTATATGATTAATAAGCTTGTACTCT 1260
QY 421 ProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
DB 1261 CTTTTTAAACCTCAAGTAAACATCTGAGACAGATTAATTTTGAATGAAGAAATTTTACA 1320
QY 441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCysMet 460
DB 1321 GCTCAGACTATTATACATTAACACACCTGAAATAATGATGAGATGTATGSACTGCAATG 1380
QY 461 AspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSerGlyArgGlu 479
DB 1381 GACATTAAGAGGCGCGCGCATTTCCCTCAATTTTCTACTCTGCAAGTGAAGAGAA 1437

RESULT 7
ADQ88265
ID ADQ88265 strand; DNA; 2811 BP.
XX
AC ADQ88265;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human 14180 DNA encodes a rac gamma Ser/Thr protein kinase RAC-PK-gamma.
KW human; gene; de; cardiovascular disorder; thrombotic disorder;
KW differential expression; gene therapy; aberrant vascularisation;
KW atherosclerosis; thrombosis; coronary artery disease; hyperlipidaemia;
KW dyslipidaemia; high blood pressure; heart failure; cardiact;
KW thrombolytic; anticoagulant; antilipemic; hypotensive; cardiant;
KW rac gamma Ser/Thr protein kinase; RAC-PK-gamma.
XX
OS Homo sapiens.
XX
PN WO2004063340-A2.
XX
PD 29-JUL-2004.
XX
PF 13-JAN-2004; 2004WO-US000393.
XX
XX 13-JAN-2003; 2003US-0439683P.
PR 05-FEB-2003; 2003US-0445216P.
PR 18-FEB-2003; 2003US-0448036P.
PR 12-MAR-2003; 2003US-0454189P.
PR 25-MAR-2003; 2003US-0457541P.
PR 29-APR-2003; 2003US-0466411P.
PR 08-MAY-2003; 2003US-0469041P.
PR 10-JUN-2003; 2003US-0477414P.
PR 13-JUN-2003; 2003US-0478560P.
PR 24-JUL-2003; 2003US-0489772P.
PR 28-JUL-2003; 2003US-0490660P.
PR 03-SEP-2003; 2003US-0499838P.
PR 22-SEP-2003; 2003US-0504786P.
PR 24-SEP-2003; 2003US-050570P.
PR 17-OCT-2003; 2003US-0512418P.
PR 27-OCT-2003; 2003US-0514660P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX

PI Steagliano NE, Healy A, Acton SL, Galvin KM, Donoghue MA;
PI Rogrigue-Way A, Tomlinson JE;
XX
DR MPI; 2004-553729/53.
DR P-PSDB; ADQ88265.

XX
XX Identifying a compound for treating a cardiovascular or thrombotic
PT disorder by combining a compound to be tested with e.g., a 9380, 9462,
PT 8701 or 2419 polypeptide or with a host cell expressing the polypeptide
PT and detecting the binding.

XX
PS Claim 1; SEQ ID NO 107; 512bp; English.

XX
XX This invention relates to a novel compound that is capable of treating a
CC cardiovascular or thrombotic disorder. Specifically, it refers to the
CC identification of nucleic acid molecules, and the encoded proteins
CC thereof, which are differentially expressed in cardiovascular disease
CC states relative to their normal expression in non-diseased tissue. The
CC present invention describes test compounds (i.e. small molecules,
CC peptides or antibodies) that can bind to and modulate the activity of
CC these differentially expressed membrane-bound polypeptides, where binding
CC is detected by a competition binding assay, immunoassay or yeast two-
CC hybrid assay. Accordingly, pharmaceutical compositions can be developed
CC and used via gene therapy to treat aberrant vascularisation,
CC atherosclerosis, thrombosis, coronary artery disease, hyperlipidaemia,
CC dyslipidaemia, high blood pressure or heart failure. As such, they
CC exhibit cardiac, thrombolytic, anticoagulant, antilipemic, hypotensive
CC and cardiac activities. This polynucleotide sequence is a human DNA
CC molecule that is differentially expressed in a patient with a
CC cardiovascular disorder, given in an exemplification of the invention.

XX
SQ Sequence 2811 BP; 905 A; 506 C; 582 G; 818 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2, 93e-258 Length: 2811
Score: 2558.00 Matches: 479
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-869-079B-3 (1-479) x ADQ88265 (1-2811)

QY 1 MetSerAspValThrIleValIysGluGlyTTPValGlnIlyAspGlyGluTyrIleIys 20
DB 1 ATGAGGAGTGTTCACATTGGAAGAAAGTGGGTTCAAGAGGAGGAGAAATATATAAAA 60
QY 21 AsnTTPArgProArgTyrPheLeuLeuLeuThrAspGlySerPheIleGlyTyrIlyGln 40
DB 61 AACTGAGGCCAAGATACCTTCCTTTGAAGACAGATGGCTCATTCATAGATATATAGAG 120
QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAspPheSerValAlaIysCysGln 60
DB 121 AAACCTCAAGATGTGGATTACCTTAATCCCTCAACAACCTTTCAATGGCAAAATGCGAG 180
QY 61 LeuMetIlySerThrGluArgProIlyProAsnThrPheIleIleArgCysLeuGlnTTPThr 80
DB 181 TTATATAAAAACAAGACCAAGCAACCAATTAATATATATATATATATATATATATATAT 240
QY 81 ThrValIleGluArgThrPheIleValAspThrProGluGluArgGluGluTTPThrGln 100
DB 241 ACTGTTATAGAGAAACATTTCTATGATATCTCCAGAGAAAGGAAAGATATGACAGAA 300
QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluGluArgMetAspCysSer 120
DB 301 GCTATCCAGGCTGTACAGACAGACTGACAGAGCAAGAAAGAGAGAAATGGAATTTGAGT 360
QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrIleHis 140
DB 361 CCAACTTCACAAATGTAT 420
QY 141 LysArgIlySerThrMetAspPheAspTyrLeuIlyLeuLeuGlyIlyGlyGlyThrPheGly 160

DB 421 AAAAAGAAAGCAATGATGATTTGACTATTGAAAATCTAGATAAGGACCTTTGGG 480
QY 161 LysValIleLeuValArgGluIlyValAspGlyIlySerTyrTyrAlaMetIlyIleIlyIys 180
DB 481 AAAGTATATTTGGTTGGAGAGAAAGGCAAGTGGAAATATATCTATCTATGAAATTCGAG 540
QY 181 LysGluValIleIleAlaIysAspGluValAlaHisThrLeuThrGlnSerArgValIleu 200
DB 541 AAAGAAAGTCAATTTTCCAAAGAGATGAGTGGACACACTTCACTGAAAGCAAGATTTTA 600
QY 201 LysAsnThrArgHisProPheLeuThrSerLeuIlySerPheGlnThrIlyAspArg 220
DB 601 AAGAACATAGACATCCCTTTTAAACATCTTGAAATATTCCTCCAGACAAAAGCCGT 660
QY 221 LeuCysPheValMetGluTyrValAlaGlnIlyGlyIlyLeuPhePheHisIleuSerArgGlu 240
DB 661 TTGCTGTTTGTGTGAAATATGTTAAATGGGGGGGAGACTGTTTTCATTTGTCGAGAGAG 720
QY 241 ArgValPheSerGlnAspArgThrArgPheTyrGlyValIleGluIleValIleSerAlaLeuAsp 260
DB 721 CGGGTGTCTCTGAGGACCGCACAGTTCATGATGAGAAATGTCTCTGCTTGAC 780
QY 261 TyrLeuHisSerGlyIlyIleValIlyArgAspLeuIlyLeuGluAsnLeuMetLeuAsp 280
DB 781 TATCTACATTCGGAAGAAATTTGTATCGGTATCTCAAGTTGAGAAATCTAATGCTGGAC 840
QY 281 LysAspGlyHisIleIlyIleThrAspPheGlyLeuCysIlyGlyIlyIleThrAspAla 300
DB 841 AAAGATGGCCACATTAATAATTCAGATTTTGGACTTTGGCAAGAGAGATCAAGATGAC 900
QY 301 AlaThrMetIlySerPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
DB 901 GCCACCATGAAAGCATTCGTGGCACTCCAGAAATATCTGCACCAAGAGGTATGAAAGAT 960
QY 321 AsnAspTyrGlyArgAlaValAspTyrTyrPyrGlyLeuGlyValValMetTyrGluMetC 340
DB 961 AATGACTAATGGCCGAGACAGATGATGCTGTGGGGCTGTAGGGGTTGATATATGAAATGAT 1020
QY 341 CysGlyIlyArgLeuProPheTyrAsnGlnAspHisIleGluIlyLeuPheGluIleuMet 360
DB 1021 TGTGGAGGTTACCTTTCTACAAACGAGACCATGAGAAACCTTTTGAATTAATTAATG 1080
QY 361 GluAspIleIlyPheProArgThrLeuSerSerAspAlaIlySerLeuLeuSerGlyLeu 380
DB 1081 GAAGACATTAATTTCTCTGAACACTCTCTTCAGATGCAAAATCATTTGCTTACGGGCTC 1140
QY 381 LeuIleIlyAspProAsnIlyAspArgLeuGlyIlyGlyProAspAspAlaIlyGlnIleMet 400
DB 1141 TTGATTAAGATCCAAATTAAGCCCTGTGTGAGAGACAGATGATCCAAAGAAATTAATG 1200
QY 401 ArgHisSerPhePheSerGlyValAsnTyrGlnAspValTyrAspIlyIlyLeuValPro 420
DB 1201 AGACACAGTTCTCTCTCGAGTAACCTGCAAGATGATATATATATATATATATATAT 1260
QY 421 ProPheIlyProGlnValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
DB 1261 CTTTTTAAACCTCAAGTAAATCTTGAGACAGATCTAGATATTTGATATAGAAATTTTAA 1320
QY 441 AlaGlnThrIleThrIleThrProProGluIlyIlyArgGluIlyAspGlyIlyMetAspCysMet 460
DB 1321 GCTCAGACTATTAATTAATTAACCACTGAAATATATATATATATATATATATATAT 1380
QY 461 AspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSerGlyIlyArgGlu 479
DB 1381 GACAAATGAGAGCGGCGCATTTCCCTCAATTTTCTACTCTGCAAGTGGAGAGAA 1437
RESULT 8
AACT77341
ID AACT77341 standard; cDNA, 3285 BP.
XX
AC AACT77341;
XX
DT 08-FEB-2001 (first entry)

XX DE Human ORFX ORF2896 polynucleotide sequence SEQ ID NO:5791.
XX
XX Human, open reading frame; ORFX, detection; cytostatic; hepatotropic;
XX vulnerray; antiparkinsonian; neurotropic; neuroprotective;
XX anticonvulsant; osteopathic; antiparkinsonian; immunosuppressant; cardiant;
XX immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
XX hypotensive; dermatological; immunosuppressive; antiinflammatory;
XX antiviral; antibacterial; antifungal; antineumatic; antihypertoid;
XX antianemic; gene therapy; cancer; proliferative disorder; hypertension;
XX neurodegenerative disorder; osteoarthritis; graft vs host disease;
XX cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
XX cholesterol ester storage; systemic lupus erythematosus; infection;
XX severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
XX allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
XX bone damage; cartilage damage; antiinflammatory disease; coagulation;
XX thrombosis; contraceptive; ss.
XX
XX Homo sapiens.
XX
XX MO200058473-A2.
XX
XX 05-OCT-2000.
XX
XX 31-MAR-2000; 2000WO-US008621.
XX
XX 31-MAR-1999; 99US-0127607P.
XX
XX 02-APR-1999; 99US-0127636P.
XX
XX 05-APR-1999; 99US-0127728P.
XX
XX 30-MAR-2000; 2000US-00540763.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinkets RA, Leach M;
XX
XX WPI; 2000-602362/57.
XX
XX P-PSDB; AAB43132.
XX
XX Novel nucleic acids and peptides derived from open reading frame X,
XX useful for treating e.g. cancers, proliferative disorders,
XX neurodegenerative disorders and cardiovascular disease.
XX
XX Claim 5; Page 4956-4958; 5507pj; English.
XX
XX AACT7446 to AAC7606 encode the proteins given in AAB40237 to AAB43397,
XX which represent the human ORFX open reading frames 1 to 3161. The ORFX
XX sequences have activities such as: cytostatic; hepatotropic; vulnerray;
XX antiparkinsonian; antiparkinsonian; neurotropic; immunostimulant;
XX anticonvulsant; antidiabetic; immunosuppressant; osteopathic;
XX cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
XX dermatological; immunosuppressive; antiinflammatory; antibacterial;
XX antiviral; antifungal; antineumatic; antihypertoid; and antianemic. The
XX sequences can be used for determining the presence of or predisposition
XX to, or preventing or treating pathological conditions associated with an
XX ORFX-associated disorder. The nucleic acids can be used to express ORFX
XX proteins in gene therapy vectors. The proteins and nucleic acids may be
XX used to treat cancers, proliferative disorders, neurodegenerative
XX disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
XX diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
XX storage, systemic lupus erythematosus, severe combined immunodeficiency
XX (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
XX disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
XX cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
XX enhance coagulation; to inhibit thrombosis; and as a contraceptive

XX SQ Sequence 3285 BP; 1028 A; 624 C; 690 G; 942 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 2, 51e-257
Score: 2550.00
Percent Similarity: 99.79%
Best Local Similarity: 99.79%
Query Match: 99.69%

Length: 3285
Matches: 478
Conservative: 0
Mismatch: 1
Indels: 0

DB: 3 Gaps: 0
US-09-869-079B-3 (1-479) x AAC77341 (1-3285)
QY 1 MetSerAspValThrIleValIysGluGlyTrpValGlnIlyAsArgGluIlyTrpIleIlys 20
DB 475 AAGACCGATGTTTACATTCATGTTGAAAGATGGGTTCCAGAAAGGAGGAAATATTAATAA 534
QY 21 AsnTPAspProArgTyrPheLeuLeuIysThrAspGlySerPheIleGlyTyrIlysglu 40
DB 535 AACTGAGGCCAAGATTCCTCTTTGAAAGACGATGGCTCTTATGATGATATTAAGG 594
QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheSerValAlaLysCysGln 60
DB 595 AAACCTCAAGATGATGATTTACCTTATCCCTCAACCACTTTTCAGTGGCAAAATGCCAG 654
QY 61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTrpThr 80
DB 655 TTAAATGAAAACGAAGCAGCAACCAAGCCAAACATTTATATCAGATGCTCCAGTGGACT 714
QY 81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluIlyTrpThrGlu 100
DB 715 ACTGTTATAGAGAAACATTTTCATGATGATCTCCAGGAAAGGAAATGACAGAA 774
QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluIlyArgMetAsnCysSer 120
DB 775 GCTATCCAGGCTGTGACAGACAGACTGCAGAGCAAGAAAGAGAGATGAAATGTAGT 834
QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSerThrThrHis 140
DB 835 CCAACTTCAAAATGATATATAGAGAGGAAAGATGAGTCCCTTCAACCAATCAT 894
QY 141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyThrPheGly 160
DB 895 AAAGAAACACATGATGATTTTTCATTTGAAATCTAGGTAAGGCACTTTTGCG 954
QY 161 LysValIleLeuValArgGluIlyLysAlaSerGlyLysTyrTyrAlaMetLysIleLeuLys 180
DB 955 AAAGTTATTTTGGTTCGAGAGAAAGGCAAGTGAATAATCTATGATGAATTCGAAAG 1014
QY 181 LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArgValLeu 200
DB 1015 AAAGAAACATATTTGCAAGATGATGAGGACACACTTAACTGAAAGCAGATATTA 1074
QY 201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
DB 1075 AAGAAACCTAGACATCCCTTTTAAATCTTGAATATTTCTTCCAGCAAAAGACGT 1134
QY 221 LeuCysPheValMetGluTyrValAsnGlyGlyIlyLeuPhePheHisLeuSerArgGlu 240
DB 1135 TTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTCCATTGTCGAGAGAG 1194
QY 241 ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGlnIleValSerAlaLeuAsp 260
DB 1195 CCGGTGTTCTCGAGAGCCGACAGCTTCTATGGGCGAAATGTCCTCCCTTGAC 1254
QY 261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
DB 1255 TATCTACATTCGGAAGATGTGTGACCTGATCTCAAGTGTGAGATTTAATGCTGGAC 1314
QY 281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIleThrAspAla 300
DB 1315 AAAGATGGCACAATAAATTCAGATTTTGGACCTTGGCAAAAGAGGATCAAGATGCA 1374
QY 301 AlaThrMetLysThrPheCysGlyLysProGluIlyTyrLeuAlaProGluValLeuGluAsp 320
DB 1375 GCCACCATGAAGACATCCCTGTGGCACTCCAGATATTCGACACAGAGGTGTTAAGAGAT 1434
QY 321 AsnAspTyrGlyArgAlaValAspTyrTrpGlyLysLeuGlyValValMetTyrGluMetMet 340
DB 1435 AATGACTATAGCCGAGCACTAGCTGTGGGCTTGAAGGCTTGTATGATTAATGATG 1494
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluIlyLysPheGluLeuIleLeuMet 360

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DB      1495  TGTGGAGAGTTACTCTTCTCAACACGACGACCACTTTGTAATTAATTTATG 1554
QY      361  GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
DB      1555  GAAGACATTAATTTCTCTCGAACACCTCTTCAGATCGAAATCATTTGCTTTCAGGGCTC 1614
QY      381  LeuIleLysAspProAlaLysValGluGlyGlyProAspAspAlaLysGluIleMet 400
DB      1615  TTGATTAAGATCCAAATTAACCGCTTGTGGAGGACCAATGATGCAAAAGAAATATG 1674
QY      401  ArgHisSerPhePheSerGlyValAsnTrpGlnAspValTyrAspLysLysLeuValPro 420
DB      1675  AGACACAGTTTCTTCTCTGAGTAACTGGACAGATTAATGATTAATTAAGCTTGTACT 1734
QY      421  ProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
DB      1735  CCTTTTAACTCCTCAAGTACATCTGACAGATCTAGATATTTTGTATGAAGAATTACA 1794
QY      441  AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCysMet 460
DB      1795  GCTCAGACTATTTCAATTAACACCACTGAATAATATGATGAGATGGTATGAGCTGCATG 1854
QY      461  AspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSerGlyArgGlu 479
DB      1855  GACAAATAGAGGCGCGCCGCACTTTCCTCAATTTTCTACTCTGCAAGTGCAGAGAA 1911

RESULT 9
AAA96637 standard; DNA; 1570 BP.
AC      AAA96637;
XX      08-FEB-2001 (first entry)
XX      DNA encoding a human Akt3 polypeptide.
DE      Human; Akt3; apoptotic cell death; apoptotic stimulating kinase 1; ASK1;
KW      hypoxia; apoptosis; necrosis; myocardial infarction; ischemia;
KW      reperfusion injury; myocardial ischemia reperfusion injury; stroke;
KW      liver damage; renal failure; organ transplantation; coronary artery; ss.
XX      Homo sapiens.
XX      OS
XX      FH      Key      Location/Qualifiers
XX      FT      CDS      126..1523
XX      FT      /*tag= a
XX      FT      /product= "Akt3"
XX      PN      MO200056866-A2.
XX      PD      28-SEP-2000.
XX      PF      14-MAR-2000; 2000MO-US006574.
XX      PR      19-MAR-1999; 99US-0125108P.
XX      PA      (AVET ) AVENTIS PHARM PROD INC.
XX      PI      Guo K, Pagnoni MF, Clark XL, Ivashchenko YD;
XX      DR      MPI, 2000-638260/61.
XX      DR      P-PSDB; AAB19011.
XX      PT      Novel Akt3 nucleic acid and proteins capable of preventing apoptotic cell
XX      PT      death induced by apoptosis stimulating kinase 1 useful for treating
XX      PT      myocardial infarction or ischemia reperfusion injury.
XX      PS      Claim 3; Page 62-64; 73pp; English.
XX      CC      The present sequence encodes a human Akt3 protein. Expression of Akt3
XX      CC      prevents apoptotic cell death induced by apoptotic stimulating kinase 1
XX      CC      (ASK1). The Akt3 polypeptide is useful for inhibiting cell death,

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CC      preferably in a cardiac myocyte, resulting from hypoxia, apoptosis or
CC      necrosis in a patient suffering from myocardial infarction or ischemia
CC      reperfusion injury. The polypeptide is also useful for treating
CC      myocardial infarction or ischemia reperfusion injury, where the
CC      reperfusion injury is myocardial ischemia reperfusion injury or is
CC      associated with stroke, liver damage, renal failure, organ
CC      transplantation or coronary artery by pass grafting
XX      SQ      Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      3,31e-242      Length:      1570
Score:      2402.00      Matches:      453
Percent Similarity:      98.91%      Conservative:      1
Best Local Similarity:      98.69%      Mismatches:      3
Query Match:      93.90%      Indels:      2
DB:      3      Gaps:      1

US-09-869-079B-3 (1-479) x AAA96637 (1-1570)
QY      1  MetSerAspValThrIleValLysGluGlyTyrValGlnLysArgGlyGlyTyrIleLys 20
DB      126  ATGAGCGATGTTTCCATTGTGAAGAAGTGGCTTCAGAAAGGCGAGAGAAATATATAAA 185
QY      21  AsnTrpArgProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGlu 40
DB      186  AACTGAGGCGCAAGATCTTCTTTGAAGACGAAGGCTCATTCATAGGATATATAAAG 245
QY      41  LysProGlnAspValAspLeuProTyrProLeuAsnAspPheSerValAlaLysCysGln 60
DB      246  AAACCTCAAGATGTGATTTACTTATCCCTCAACACTTTCACTGGCAAAATGCGAG 305
QY      61  LeuMetLysThrGluArgProLysProAsnThrPheIleLeuArgCysLeuGlnTrpThr 80
DB      306  TTAATGAAAACAGAAAGACCAAGACCAACATTTATATCATGATGTCCTCAGTGGACT 365
QY      81  ThrValIleGluArgThrPheHisValAspThrProGlnGluArgGluGlnTrpThrGlu 100
DB      366  ACGTTATAGAGAACATTTCATGTAGATATCCAGAGAAAGGAAAGATGACAGAA 425
QY      101  AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluLysArgMetAsnCysSer 120
DB      426  GCTATCCAGGCTGTACAGACAGACTGCAAGGCGCAAGAGAGAGAGAAATTTAGT 485
QY      121  ProThrSerGlnIleLeuPheAsnIleGlyGluGlnGluMetAspAlaSerThrHisHis 140
DB      486  CCAACTTCACAAATGATATATATAGAGAGAAAGATGGATGCTCTACAAACCCATCAT 545
QY      141  LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyThrPheGly 160
DB      546  AAAAGAAAGCAATGATGATTTTGTACTATTGAAACTATAGTAAAGGCACTTTGGG 605
QY      161  LysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAlaMetLysIleLeuLys 180
DB      606  AAGTTATTTTGGTTCGAGAGAGGCAAGGCAAAATATCATTCATGAAATTCGAAAG 665
QY      181  LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGlnSerArgValLeu 200
DB      666  AAAGAAGTCATATTTCACAAAGATGAAGTGSCACACACTTAAGTAAGCAAGATATTA 725
QY      201  LysAsnThrArgHisPhePheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
DB      726  AAGAACATAGACATCCCTTTTAAACATCTTGAATAATTTCTTCAGAGAAAGACCGT 785
QY      221  LeuCysPheValMetGlyTyrValAsnGlyGlyLysLeuPhePheHisLeuSerArgGlu 240
DB      786  TTGTGTTTGTGATGATATGATTTATGGGGGAGACTGTTTTCATTTGTGAGAGAG 845
QY      241  ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAlaLeuAsp 260
DB      846  CGGGTGTCTCTGAGACGSCACACGTTTCTAATGAGGCAAAATGTCCTGCTGGCTGAC 905
QY      261  TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuValuAsnLeuMetLeuAsp 280

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Db      906 TATCTACATTCGCGAAGATGTGTACCGGATCTCAAGTTGAGAAATCTAATGTCGAGC 965
QY      281 LysAspGlyHisIleIleValIleThrAspGlyLeuGlyGluGlyIleThrAspAla 300
Db      966 AAGATGGCCACATTAATAATTAACAGATTGTGACTTTGCAAGAGAGATCAACAGATGCA 1025
QY      301 AlaThrMetIleThrPheCysGlyThrProGluTyrLeuAlaProGluValIleGluAsp 320
Db      1026 GCCACCATGAAAGCATTTCTGTGCACTCCAGAAATATCTGGACCAAGGTGTTAGAAAGT 1085
QY      321 AsnAspTyrGlyValArgAlaValAspTyrPheGlyLeuGlyValValMetTyrGluMet 340
Db      1086 AATGACTATAGCCGACAGACAGTACTGTGGGCGCTTGGAGGTGTCTCATGTATGAATGATG 1145
QY      341 CysGlyValGluLeuProGlyThrPheGlyValGluGlyLeuGlyLeuGlyLeuMet 360
Db      1146 TGTGGAGAGGTACCTTTCTTCAACACGAGACATGAGAACTTTTGAATTTAAATTAAGT 1205
QY      361 GluAspIleIleAspPheProArgThrLeuSerSerAspAlaIleSerLeuLeuSerGlyLeu 380
Db      1206 GAAAGCATTTAAATTTCTGCAACACTCTCTTCAGATGCAAAATCATTTGCTTTAGGGCTC 1265
QY      381 LeuIleLysAspProAsnLysArgLeuGlyGlyIleProAspAspAlaIleGlyIleMet 400
Db      1266 TTGATTAAGAGATCCAAATAAAACCTTGTGGAGACACAGATGATGCAAAAGAAATTAAG 1325
QY      401 ArgHisSerPhePheSerGlyValAlaThrProGluAspValTyrAspLysLeuValPro 420
Db      1326 AGACACAGATTTCTTCTGTGAGTAACTGTGCAAGATGATATATATAAAAGCTTGTACCT 1385
QY      421 ProPheLysProGluValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
Db      1386 CTTTAAACCTCAAGTAACTCTGACACGATCTGATGATTTTGTATGAAGATTTTAC 1445
QY      441 AlaGluThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCys 459
Db      1446 GCTCAGACTATTAACAATAACACACACCTGAAATAATGTCAGCAATCA-----GATGT 1496

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RESULT 10
AAH79025
ID AAH79025 standard; cDNA; 1570 BP.
XX
XX AAH79025;
AC
XX
DT 31-JAN-2002 (first entry)
XX
DE Human Akt3 encoding cDNA SEQ ID NO 1.
XX
DE Human; Akt3; AH/PH-domain containing serine/threonine kinase; Akt;
KW cerebroprotective; neurotrophic; hepatotrophic; inhibitor of apoptosis; ASK1;
KW osteopapnic; vasotrophic; hepatotrophic; inhibitor of apoptosis; ASK1;
KW apoptosis stimulating kinase 1; hypoxia; necrosis; myocardial infarction;
KW ischemia reperfusion injury; stroke; organ transplantation;
KW coronary artery bypass; tumour cell survival; gene therapy;
KW Alzheimer's disease; osteoarthritis; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 126..1523
FT /*tag= a
FT /product= "Akt3"
FT
XX
XX PN MO200168850-A2.
XX
XX 20-SEP-2001.
XX
XX 09-MAR-2001; 2001MO-US007663.
XX
XX 14-MAR-2000; 2000US-00526043.
XX
XX (AVET) AVENTIS PHARM PROD INC.

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XX      XX Guo K, Pagnoni MF, Clark KL, Ivashchenko YD;
PI      DR MPI; 2001-582452/65.
XX      DR P-PSDB; AAG78018.
XX      PT New nucleic acid encoding human Akt3 protein, useful for inhibiting cell
PT      death and treating myocardial infarction, ischemia reperfusion injury
PT      associated with stroke, liver damage and renal failure.
XX      PS Claim 1, Page 59-62; 73pp; English.
XX      CC The invention relates to human Akt3 protein (AH/PH-domain containing
CC      serine/threonine kinase, Akt) comprising a fully defined sequence
CC      (AAG78018) of 465 amino acids, its splice variant or allelic variant,
CC      where the encoding polynucleotide hybridises under stringent conditions
CC      with a nucleic acid containing a nucleotide sequence (AAH79025) of 1570
CC      base pairs defined in the specification. Akt3 has cerebroprotective,
CC      neurotrophic, hepatotrophic, antiarthritic, osteopapnic, vasotrophic and
CC      hepatotrophic activity, as an inhibitor of apoptosis and/or apoptosis
CC      stimulating kinase 1 (ASK1)-induced cell death. Akt3 operably linked to a
CC      regulatory region is useful for inhibiting cell death in cardiac myocytes
CC      resulting from hypoxia, apoptosis or necrosis and for treating myocardial
CC      infarction or ischemia reperfusion injury, particularly that associated
CC      with stroke, liver damage, renal failure, organ transplantation or
CC      coronary artery bypass grafting. Agonist of Akt3 are useful for improving
CC      Akt3 activity during treatment of patients suffering from myocardial
CC      infarction or ischemia reperfusion injury and inhibitors of Akt3
CC      activity decrease tumour cell survival and result in tumour regression.
CC      Akt3 protects cells from apoptosis. Gene therapy using Akt3 reduces the
CC      quantity of cell death and final infarct size, resulting in improved post
CC      -infarction function, improved quality of life and reduced mortality. In
CC      patients with existing heart failure, gene therapy with Akt3 retards the
CC      process of ventricular dilation and slows down disease progression. Akt3
CC      gene therapy is useful for treating other disease states, involving cell
CC      death by apoptosis, including Alzheimer's disease, liver degeneration or
CC      osteoarthritis
XX      SO Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;

```

Alignment Scores:
Pred. No.: 3,31e-242 Length: 1570
Score: 2402.00 Matches: 453
Percent Similarity: 98.91% Conservatve: 1
Best Local Similarity: 98.69% Mismatches: 3
Query Match: 93.90% Indels: 2
DB: 4 Gaps: 1

US-09-869-079b-3 (1-479) x AAH79025 (1-1570)

```

QY      1 MetSerAspValThrIleValGlyGluGlyTyrPValGlnLysArgGlyGluTyrIleLys 20
Db      126 ATGAGGAGATGTTACCTTGTGAAGAGGTGGGTTCACAAAGGGGAGAAATATATATAA 185
QY      21 AsnTyrArgProArgGlyThrPheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGlu 40
Db      186 AACTGAGGCCCAAGATACCTTCTTTGAAGACAGATGCTCATTCATCAGATATATAAGG 245
QY      41 LysProGluAspValAspLeuProTyrProLeuAsnAspSerValAlaLysCysGln 60
Db      246 AAACCTCAAGATGTGATTTACCTTATCCCTCAACAACCTTTTCAGTGGCAAAATGCCCAG 305
QY      61 LeuMetLysThrGluArgProLysProLeuThrPheIleIleArgCysLeuGlnTyrPheThr 80
Db      306 TTAATGAAACACAGACGACCAAGCCAAACACATTTATATACAGATGTCCAGGTGACT 365
QY      81 ThrValIleGluArgThrPheHisValAlaAspThrProGluGluArgGluGluTyrPheThr 100
Db      366 ACTGTTATGAGAGAACTTTCTATGATGATCTCCAGAGAGAAAGGAAATGACAGAA 425
QY      101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluGluArgLysSerSer 120
Db      426 GCTATCAGGCTGTGTGACAGACAGACTGCAGAGGCAAGAGAGAGATGATGTAGT 485

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QY 121 ProthSerGlnIleAspAsnIleGlyGluGluMetAspAlaSerThrThrHis 140
DB 486 CCACTTCACAAATGATTAATATAGAGAGAGAAAGATGGATGCTCTACCAACCATCAT 545
QY 141 LysArgIleThrMetCysAspPheAspTyrLeuLysLeuGlyLysGlyThrPheGly 160
DB 546 AAAAGAAAGCAATGATGATTTTGAATATTGAACTACTAGTAAAGCAGCTTTGGG 605
QY 161 LysValIleLeuValAlaGlyLysAlaSerGlyLysTyrTrpAlaMetLysIleLeu 180
DB 606 AAAGTTATTTGGTTCCAGAGAAAGGCAAGCAAAATACATAGCTATGAAAGATCTGAAG 665
QY 181 LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArgValLeu 200
DB 666 AAAGAGCTCATATTATGCAAAAGATGAGTGGCACACCTCTAAGTGAACGACAGATATTA 725
QY 201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
DB 726 AAGAACCTAGACATCCCTTTTAACTCCTTGAAATATTCCTTCCAGACAAAAGACCTG 785
QY 221 LeuCysPheValMetGlyTyrValAsnGlyGlyGluLeuPhePheHisLeuSerArgGlu 240
DB 786 TTGGTTTGTGATGGAATATGTTAATGGGGGCAAGCTGTTTCCATTTGTCGAGAGAG 845
QY 241 ArgValPheSerGluAspArgThrArgPheTyrGlyValAlaGluIleValSerAlaLeuAsp 260
DB 846 CGGGTGTCTCTGAGGAGCCGACAGCTTCTATGAGTCAAAATATGCTGCTGCTGGAC 905
QY 261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
DB 906 TATCTCATATCCGGAAGATTTGTGTACCCGTGATCTCAAGTTGGAGATCTAAATGCTGGAC 965
QY 281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCysArgGlyLysIleThrAspAla 300
DB 966 AAAGATGGCCACATAAATTAATGAGATTTTGACCTTGCAAAAGAGGATCACAGATGCA 1025
QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
DB 1026 GCCACCATGAAAGCATTTCTGTGCACCTCCAGAAATATCTGGCACACAGGGTGAAGAAT 1085
QY 321 AsnAspTyrGlyArgAlaValAspTrpTrpGlyLeuGlyValValMetTyrGluMetMet 340
DB 1086 AATGACTATGCGGAGAGAGTGTGTGGGCTTACGGGTTGTCAATGATGAATGATG 1145
QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGluLeuIleLeuMet 360
DB 1146 TGTGGGAGGTTACCTTTCTCAACACAGGACCATGAGAAACTTTTGAATTAATTAATG 1205
QY 361 GluAspIleLysPheProAlaGlnThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
DB 1206 GAAGACATTAATTTCTCTCAACACCTCTCTTCAGATGCCAAATCATTTGACGGGCTC 1265
QY 381 LeuIleLysAspProAsnLysArgLeuGlyGlyProAspAspAlaLysGluIleMet 400
DB 1266 TTATATTAAGATCCAAATTAACCGCTTGTGAGAGACCAATGATGCAAAAGAAATTAAG 1325
QY 401 ArgHisSerPhePheSerGlyValAsnTrpGlnAspValTyrAspLysLysLeuValPro 420
DB 1326 AGACACAGTTTCTCTCTGAGTAACCTGGCAAGATGTAATGTAATAAAAGCTTGTATCCT 1385
QY 421 ProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
DB 1386 CCTTTTAAACCTCAAGTACATCTGAGACAGATACATGATATTTTGTATGAAGATTTTACA 1445
QY 441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCys 459
DB 1446 GCTCAGACTATTACATTAACCACTGAAATAAATGTCAGCAATCA-----GATTGT 1496

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RESULT 11
AAA89264
ID AAA89264 standard; cDNA; 1570 BP.
XX

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AC AAA89264;
DT 28-MAR-2001 (first entry)
XX
DE Human serine/threonine protein kinase Akt3 cDNA.
KW Akt3; human; protein kinase; vascular endothelial growth factor; VEGF;
KW inducer; ischemia; cardiomyopathy; angiogenesis; tumour; gene therapy;
KW ss.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 126..1523
FT /tag= a
XX
PN MO200077190-A2.
XX
PD 21-DEC-2000.
XX
PF 01-JUN-2000; 2000MO-US015098.
XX
PR 11-JUN-1999; 99US-0138724P.
PR 03-NOV-1999; 99GB-00026058.
XX
PA (AVERT ) AVENTIS PHARM PROD INC.
XX
XX Guo K, Ivashchenko Y, Clark K;
XX
XX WPI: 2001-025336/03.
XX
XX P-PSDB; AAB19996.
XX
PT Inducing expression of vascular endothelial growth factor, useful for
PT treating an ischemic condition, e.g. cerebrovascular ischemia, renal
PT ischemia or pulmonary ischemia, comprises administering a
PT serine/threonine protein kinase Akt protein.
XX
XX Example 1; Page 55-58; 67pp; English.
XX
XX The present sequence is that of cDNA coding for human Akt3 (see
XX AAB19996), a novel Akt isoform. Akt3 is a serine/threonine protein kinase
XX capable of inducing vascular endothelial growth factor (VEGF) expression.
XX The sequence was deduced from 2 cDNA clones isolated from a human heart
XX cDNA library using a human Akt3 partial clone as probe. Akt3 is shorter
XX than Akt1 (see AAB19997) and Akt2 (see AAB19998) and there is no
XX significant homology between Akt3 and Akt1 or Akt2 at the C-terminus of
XX the molecules. A claimed method of inducing expression of VEGF in a cell
XX involves administering Akt1, Akt2 or Akt3, or a nucleic acid encoding
XX such a protein. The cell is preferably from a patient suffering from an
XX ischemic condition, especially cerebrovascular, renal, pulmonary, limb
XX or myocardial ischemia, or ischemic, idiopathic or hypertrophic
XX cardiomyopathy. The result is beneficial collateral blood vessel
XX formation. A claimed method of inhibiting angiogenesis in a patient
XX suffering from a tumour, comprises inhibiting the level of Akt activity
XX in the patient, thereby inhibiting production of VEGF. The method
XX comprises introducing an Akt antisense nucleic acid, an intracellular
XX binding protein (e.g. a scFv) that specifically binds the Akt protein, or
XX a nucleic acid encoding a dominant negative form of an Akt
XX
XX Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;

```

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

3,31e-242

2402.00

98.91%

98.69%

93.90%

4

1570

453

1

3

2

1

1

1

1

1

Db 126 ATGAGCATGTTACCATTTGTGAAGAAGGTTGGGTTCAAGAGGAGGAGAAATATATATAA 185
 QY 21 AANTPARGProArghrPhrheuleuYrThrAspGlySerPheIleGlyTyrIleuVal 40
 Db 186 AACTGAGAGCCAGAGACTTCTTTTGAAGACAGATGGCTCATTCATAGAGATATATAAG 245
 QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheSerValAlaLysCysGln 60
 Db 246 AAACCTCAAGATGTGGATTACTTATCCCTCAACACACTTTTCAGTGGCAAAATCCAG 305
 QY 61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTyrPthr 80
 Db 306 TTTAATGAAAACAGAAAGACCAACCAACATTTATATCATGAGTGTCCAGTGGAGCT 365
 QY 81 ThrValIleGluArgThrPheHisValAspThrProGluGluLysGluGluTyrPthrGlu 100
 Db 366 ACTGTTATAGAGAACATTTTCATGTAGATCTCCAGAGAGAAAGGAAAGATGACAGAA 425
 QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluLysArgMetAsnCysSer 120
 Db 426 GCTATCCAGGCTGTAGACAGACTGACAGAGCAGAAAGAGAGAGATGAAATGTAATGTA 485
 QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrHis 140
 Db 486 CCAACTTCACAAAATTGATATATAGAGAGAGAGATGATGCTCTCAACCCATCAT 545
 QY 141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuGluLysGlyThrPheGly 160
 Db 546 AAAAGAAAGCANTGATGATTTTGTACTTTTGAACCTAGTAAAGGCACTTTTGG 605
 QY 161 LysValIleLeuValArgLysLysAlaSerGlyLysTyrTyrAlaMetLysIleLeuLys 180
 Db 606 AAAGTATTTTGGTGTGAGAGAGAGCAAGTGGAAATATCATGCTATGAAATTCGAAG 665
 QY 181 LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArgValLeu 200
 Db 666 AAAGAGTCATATATTCGAAAGATGAGAGTGGCACACACTTCAAAAGCAGAGATTA 725
 QY 201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
 Db 726 AAGAACACTAGACATCCCTTTTAAACATCTTGAAATATCTCTCCAGCAAAAGCCGT 785
 QY 221 LeuCysPheValMetGluTyrValAlaGlnGlyGluLeuPhePheHisIleuSerArgGlu 240
 Db 786 TTGTGTTTGTGATGGAATATGTTAATGGGGGAGACTGTTTTCATTTGTGAGAGAG 845
 QY 241 ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAlaLeuAsp 260
 Db 846 CCGGTGTTCTTGAGAGACGACACGTTCTATGTGAGAAATTTGCTCTGCTTGAC 905
 QY 261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
 Db 906 TATCTACATTCGAGAAAGATTTGTATCCGTGATCTCAAGTTGAGAAATCTTAATGCTGAC 965
 QY 281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCysIleGluGlyIleThrAspAla 300
 Db 966 AAAGATGGCCACATAAAATTAACAGATTTTGAAGCTTTGCAAAAGAGATCAAGATGCA 1025
 QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
 Db 1026 GCCACCATAGAACATTCGTGTGCACTCCAGAAATATCTGGCACCAAGGGTTTAAAGAT 1085
 QY 321 AsnAspTyrGlyArgAlaValAspTyrPThrGlyLeuGluValValMetTyrGluMetCmet 340
 Db 1086 AATGACTATGGCCGAGACAGTACGCTGTGGGGCTTGAGGGGTTTCATGATGAAATGATG 1145
 QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleuMet 360
 Db 1146 TGTGGAGAGTTACTTTTCAACACAGACCATGAGAACTTTTGAATTAATTAATTAAG 1205
 QY 361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLysGlyLeu 380
 Db 1206 GAAGACATTAATTTCTCTGAAACATCTCTTCAGATGCAAAATCATTTGCTTTCAGGGCTC 1265

QY 381 LeuIleLysAspProAsnLysArgLeuGlyGlyGlyProAspAspAlaLysGluIleuMet 400
 Db 1266 TTGATTAAGGATCCAAATTAACGCTTGTGGAGAGACAGAGATGCAAAAGAAATTAAG 1325
 QY 401 ArgHisSerPhePheSerGlyValAsnThrGlnAspValTyrAspLysIleValPro 420
 Db 1326 AGACACAGATTTCTCTGTGAGTAACTGGCAAGATGTATATGATTAATAAAGCTTGACCT 1385
 QY 421 ProPheLysProGluValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
 Db 1386 CCTTTAAACCTCAAGTAACTGTAGACAGTACTAGATATTTGATGTAAGAAATTTACA 1445
 QY 441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCys 459
 Db 1446 GCTCAGACTATACATATAACACACTGAAAAATGTACAGATCA-----GATTGT 1496
 RESULT 12
 ADG85244
 ID ADG85244 standard; DNA; 1570 BP.
 XX
 AC ADG85244;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human Chrysoosporium associated DNA.
 XX
 KW de; gene; beta-glucosidic bond; beta-xylosidic bond; human.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 126..1523
 FT /tag= a
 FT /product= "Chrysoosporium associated protein"
 XX
 PN US2004002136-A1.
 XX
 PD 01-JAN-2004.
 XX
 PF 21-MAR-2003; 2003US-00394568.
 XX
 PR 06-OCT-1998; 98WO-EP006496.
 PR 06-OCT-1999; 99WO-NL000618.
 PR 13-APR-2000; 2000US-00548938.
 XX
 PA (EMBL/) EMBLFRB M. A.
 PA (BURL/) BURLINGAME R. P.
 PA (OLSO/) OLSON P. T.
 PA (SINI/) SINITSYN A. P.
 PA (PAR/) PARICHE M.
 PA (BOUS/) BOUSSEN J. C.
 PA (PYNN/) PYNNONEN C. M.
 PA (PUNT/) PUNT P. J.
 PA (VZEL/) VAN ZEIJL C. M. J.
 XX
 PI Email:arb MA, Burlingame RP, Olson PT, Sinitsyn AP, Pariche M;
 PI Bousson JC, Pynnönen CM, Punt PJ, Van Zeijl CMJ;
 XX
 DR WPI; 2004-061663/06.
 DR P-PSDB; ADG85245.
 XX
 PT Novel mutant Chrysoosporium strain comprising nucleic acid sequence
 PT encoding polypeptide of interest such as proteases and lipases, the
 PT nucleic acid sequence being operably linked to expression-regulating
 PT region.
 XX
 PS Disclosure; SEQ ID NO 1; 70bp; English.
 PS
 CC The invention relates to a mutant Chrysoosporium strain comprising a
 CC nucleic acid sequence encoding a polypeptide of interest. A mutant
 CC Chrysoosporium strain is useful for producing a polypeptide of interest by
 CC culturing a mutant Chrysoosporium strain under conditions permitting

expression of the protein or polypeptide, and recovering the subsequently produced polypeptide of interest. The conditions further permit secretion of the protein or polypeptide of interest. The polypeptides are useful for hydrolysing beta-glucosidic bonds. A polypeptide is useful for hydrolysing beta-xyloisidic bonds. The present sequence represents human Chrysoosporium associated DNA.

XX Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3..j1e-242	Length:	1570
Score:	2402.00	Matches:	453
Percent Similarity:	98.91%	Conservative:	1
Best Local Similarity:	98.69%	Mismatches:	3
Query Match:	93.90%	Indels:	2
DB:	12	Gaps:	1

US-09-869-079B-3 (1-479) x ADG85244 (1-1570)

QY 1 MetSerAspValThrIleValIySGluGlyTTPValGlnIyAspGlyGlyTyrIleIyS 20
 DB 126 ATGAGGAGATGTTCATTTGAAAGAGGTTGGGTTCAAGAGGGGAGAAATATATATAA 185
 QY 21 AsnTTPArgProArgTyrPheLeuLeuIyThAspGlySerPheIleGlyTyrIySGlu 40
 DB 186 AACTGAGGCCAGATACCTTCCTTTGAGACAGATGGCTCATTCATAGATTAAGAG 245
 QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAspPheSerValAlaIyS 60
 DB 246 AAACCTCAAGATGTGGATTACCTTATCCCTCAACACTTTTCAAGGGCAAAATGCGAG 305
 QY 61 LeuMetIyThThrIleuArgProIySProAsnThrPheIleIleArgCysLeuGlnTTPThr 80
 DB 306 TTATATATAACAGAACAGACCAAGCCAAACATTTATATACAGATGTCCAGTGAGACT 365
 QY 81 ThrValIleGluIyThrPheHisValAspThrProGluIyIySGluGlyTTPThrGlu 100
 DB 366 ACTGTTATAGAGAACTTTCATGTAGATCTCCAGAGAAAGGAGAAATGACAGAA 425
 QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnIySGluGlyIySGluIySGluIySGlu 120
 DB 426 GCTATCCAGGCTGTAGACAGACAGCTGAGAGGCAAGAGAGAGAAATGTAATGTAAG 485
 QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluIySGluIySGluIySGluIySGlu 140
 DB 486 CCAACTTCACAAATTTGATATATAGAGAGAGAGATGATCCCTTACACCCATCAT 545
 QY 141 LysArgIyTherMetAspPheAspTyrLeuIySGluIySGluIySGluIySGluIySGlu 160
 DB 546 AAAGAAAGCAATGATGATTTTGAATTTTGAACCTACTAGATTAAGGACCTTTGGG 605
 QY 161 LysValIleLeuValIySGluIySGluIySGluIySGluIySGluIySGluIySGlu 180
 DB 606 AAAGTATTTTGGTGTGAGAGAGGCAAGTGAAGAAATACATCTATGAAGATTCGAG 665
 QY 181 LysGluValIleIleIleIyAspGluValAlaHisThrIleuThrGluSerArgValLeu 200
 DB 666 AAAGAAGTCATTTTCACAAAGATGAGAGGACACACTTAACTGAAGCAAGATATTA 725
 QY 201 LysAsnThrArgHisPheProPheLeuThrSerLeuIySGluIySGluIySGluIySGlu 220
 DB 726 AAGAAACATAGACATCCCTTTTAAACATCCCTTGAATATTCCTTCAGACAAAAGACCG 785
 QY 221 LeuCysPheValMetGluTyrValIySGluIySGluIySGluIySGluIySGluIySGlu 240
 DB 786 TTGTGTTTGTGATGGAATATGTTAAATGGGGGCGAGCTGTTTTCATTTGTGAGAGAG 845
 QY 241 ArgValIyPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAlaLeuAsp 260
 DB 846 CGGGTGTCTCTAGAGACCGACACGTTCTATGGGACAAATTTGCTTGGCTTGGAC 905
 QY 261 TyrLeuHisSerGlyIySGluIySGluIySGluIySGluIySGluIySGluIySGluIySGlu 280

DB 906 TATCTACATTCGCGAAAGATGTGTACCGGATCTCAAGTTGGAGAAATCTATGCTGAC 965
 QY 281 LysAspGlyHisIleIySGluIySGluIySGluIySGluIySGluIySGluIySGluIySGlu 300
 DB 966 AAAGATGGCCACATTAATAATTCAGATTTTGGACTTTGCAAGAAAGAGATCACAGATGCA 1025
 QY 301 AlaThrMetIyTherPheCysGlyThrProGluIyTyrLeuAlaProGluValLeuGluAsp 320
 DB 1026 GCCACCATTAAGACATTCCTGTGGCACTCCAGATATCTGGACACAGAGGTTTGAAGAT 1085
 QY 321 AsnAspTyrGlyArgAlaValAspTTPArgIySGluIySGluIySGluIySGluIySGluIySGlu 340
 DB 1086 AATGATTAATGGCCGAGACATTAAGCTGTGGGGCTTATGGGTTGTATGATTAATGATG 1145
 QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluIySGluIySGluIySGluIySGluIySGlu 360
 DB 1146 TGTGGAGGGTTACCTTCTTACAAACGAGACCATGAGAACTTTTGAATTAATTAAG 1205
 QY 361 GluAspIleIyPheProArgThrIleuSerSerAspAlaIySGluIySGluIySGluIySGlu 380
 DB 1206 GAAGACATTAATTTCTCTGAACACTCTCTCAGATGCAAAATCATTCCTTCAAGGCTC 1265
 QY 381 LeuIleIyAspProAsnIySGluIySGluIySGluIySGluIySGluIySGluIySGluIySGlu 400
 DB 1266 TTGATTAAGATCCAAATTAAGCCTTGTGGAGAGCCAGATGATCCAAAGAAATTAAG 1325
 QY 401 ArgHisSerPhePheSerGlyValAsnTTPGlnAspValIySGluIySGluIySGluIySGlu 420
 DB 1326 AGACACAGTTCTCTCTGAGTAACTGGCAAGATGATATGATTAATAAGCTTGTACCT 1385
 QY 421 ProPheIySGluIySGluIySGluIySGluIySGluIySGluIySGluIySGluIySGluIySGlu 440
 DB 1386 CTTTAAACCTCAAGTAACTGTGACAGATCTAGATATTTGATTAAGATTAATTA 1445
 QY 441 AlaGlnThrIleThrIleThrProProGluIyTyrAspGluAspGlyMetAspCys 459
 DB 1446 GCTCAGACTTATTAACATTAACACCACTGAAATAATGTCACATCA-----GATTGT 1496

RESULT 13
 ADNT1941
 ID ADNT1941 standard; cDNA; 2277 BP.
 XX
 AC ADNT1941;
 DE
 DT 12-AUG-2004 (first entry)
 XX
 XX Chicken serine/threonine protein kinase (akt1) encoding cDNA SEQ ID:27.
 KW kinase pathway inhibitor; anti-prostate cancer;
 KW mitogen-activated protein kinase pathway inhibitor;
 KW MAP kinase pathway inhibitor; prostate cancer inhibitor;
 KW phosphatidylinositol 3-kinase/akt kinase pathway;
 KW PI3K/Akt kinase pathway; cytosolic; MAP kinase inhibitor;
 KW phosphatidylinositol 3-kinase/akt kinase inhibitor;
 KW PI3K/Akt kinase inhibitor; androgen receptor inhibitor; prostate cancer;
 KW chicken; serine/threonine protein kinase; akt1; gene; ss.
 XX
 OS Gallus gallus.
 XX
 FH Key Location/Qualifiers
 FT CDS 466..1398
 FT /cseg a
 FT /product= "serine/threonine protein kinase (akt1)"
 PD MO2004041185-A2.
 XX
 XX 21-MAY-2004.
 XX
 XX 31-OCT-2003; 2003WO-US034636.
 XX
 XX 31-OCT-2002; 2002US-0423340P.
 XX
 PA (UNRP) UNIV ROCHESTER.

XX Chang C, Lee Y, Lin W;
PI MPI: 2004-390508/36.
DR P-PSDB; ADN71942.
XX
PT Composition useful in the treatment of e.g. prostate cancer comprises a
PT kinase pathway inhibitor and an anti-prostate cancer compound.
XX
PS Disclosure; SEQ ID NO 27; 118bp; English.
XX
XX The present invention describes a composition (C1) which comprises a
CC kinase pathway inhibitor (a) and an anti-prostate cancer compound (b).
CC Also described: (1) identification of a mitogen-activated protein (MAP)
CC kinase pathway inhibitor involving incubating an androgen or a
CC library of molecules with a cell containing an activable MAP kinase
CC pathway and selecting the molecules which inhibit the activation of the
CC MAP kinase pathway; and (2) identification of a prostate cancer inhibitor
CC involving incubating a cell with hydroxyflutamide and potential
CC phosphatidylinositol 3-kinase (PI3K)/Akt kinase pathway or
CC cytoskeletal activity, and can be used as a MAP kinase inhibitor,
CC phosphatidylinositol 3-kinase (PI3K)/Akt kinase inhibitor, and androgen
CC receptor (AR) inhibitor. C1 can be used in the treatment of prostate
CC cancer; for identifying a MAP kinase pathway inhibitor; for identifying a
CC prostate cancer inhibitor; and for reducing the number of prostate cancer
CC cells in a sample. The composition C1 provides effective combination
CC therapy as compared to prior therapies. The present sequence encodes
CC chicken serine/threonine protein kinase (akt1), which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 2277 BP; 672 A; 490 C; 549 G; 566 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 3,95e-215 Length: 2277
Percent Similarity: 2146.50 Matches: 404
Best Local Similarity: 91.25% Conservative: 34
Query Match: 84.17% Mismatches: 37
DB: 83.91% Indels: 5
Gaps: 4
US-09-869-079b-3 (1-479) x ADN71941 (1-2277)
QY 1 MetSerAspValThrIleValysGluGlyTyrIleValGlnLeuSerGlyGluTyrIleLeu 20
DB 466 ATGAATGAAGTACGATGAGTGAAGAGATGGCTCCACAAAGAGAGATATATCAAA 525
QY 21 AsnTTPArgProArgTyrPheIleuLeuLeuYsthrAspGlySerPheIleGlyTyrIleGlu 40
DB 526 ACATGAGGCGACGATATTTCTTTTAAAGATGATGACATTCATTGGCTACAGGAA 585
QY 41 LysProGlnAspValAsp---LeuProTyrProLeuAsnAsnPheserValAlaLysCys 59
DB 586 CGACCCCAAGACCTTACCAACAGAAATCACTTTAAATTAATCTTCAGTAGCTCAGTGC 645
QY 60 GlnLeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTyr 79
DB 646 CAGCTATGAAGCAAGACGACCTTAACCAACATTTATCTTATGATGCGCTCCAGTGG 705
QY 80 ThrThrValIleGluArgThrPheHiseValAspThrProGluGluArgGluTyrPthr 99
DB 706 ACCACAGTATGAAAGAAACATTCATGAGACCTCCAGAGAGCGGAGAAAGATGACA 765
QY 100 GluAlaIleGlnAlaValAlaAspArgLeuGlnArgGluGluGluLysArgLysCys 119
DB 766 AAGGCTATCCAACTTTGACAGACCTCCACAGAAACAGAGAAAGATGATGATTTT 825
QY 120 SerProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrHis 139
DB 826 AAGATCGGTCTCTCTAGTATATTCAGGTGCTGAAGAAATGAAATTTCTATGACAAG 885
QY 140 HisLysArgLys---ThrMetAsnAspPheAspTyrIleuLysLeuGluGlyLysGlyThr 158

DB 886 CCAAAACAAAGTACCATGATGATTTGAATACCTTAAGCTACGTGGAAAAGGCACT 945
QY 159 PheGlyLysValIleLeuValArgLysLysAspGlyLysTyrThrAlaMetLysIle 178
DB 946 TTTGGAAAGCTATTTTACTTAAAGAAAAGCAACCGACGGTATTTATGCTATGAAAATT 1005
QY 179 LeuLysLysGluValIleIleAlaLysAspGluValAlaHiseThrLeuThrGluSerArg 198
DB 1006 CTGAAGAAAGAAAGTATTGTAGCAAAAGATGAAATGACACACGCTGACAGAAAACGTT 1065
QY 199 ValLeuLysAsnThrArgHisePheLeuThrSerLeuLysTyrSerPheGlnThrLys 218
DB 1066 GTTTTACAGAACTCAGCGGATTCATCTTAACAGCTTTAAAGTATCTTTTCAGACACAC 1125
QY 219 AspArgLysCysPheValMetGluTyrValaGngLysGluLeuPhePheHiseSer 238
DB 1126 GATCGCTGT 1185
QY 239 ArgGluArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAla 258
DB 1186 AAGAGACGCTGATTTTTCGAAAGACCGGGCGCTTTTATGGGGCTGAGATTGTTTCAGCG 1245
QY 259 LeuAspTyrLeuHiseSerGlyLys---IleValTyrArgAspLeuLysLeuGluAsnLeu 277
DB 1246 CTGAGTTACCTGCATTCAGAGAAAGATGGTGTGACAGGATTTGAAGCTGAAAATCTT 1305
QY 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCysLeuGlyIle 297
DB 1306 ATGCTGATTAAGACGGGACATTAATAATTACAGACTTTGGACTTGTAAAGAGGACAT 1365
QY 298 ThrAspAlaIleThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluVal 317
DB 1366 AAGATGAGCAACATGAAAGCTTCTGTGCACTCCAGAGTATCTTGACACAGAGGTG 1425
QY 318 LeuGluAspAsnAspTyrGlyArgAlaValAspTyrPthrGlyLeuGlyValValMetLys 337
DB 1426 CTGGAGGATTAAGAACTATGATGATTCACGCACTTGTGCTCAGGAAACAAATCTCTTG 1485
QY 338 GluMetMetCysGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGluLeu 357
DB 1486 GAAATGATGTGTGGCGGCTCCCTTTCTACATCCAGACCATGAAAGCTCTTTGAATCTC 1545
QY 358 IleLeuMetGluAspIleLysPheProArgThrIleSerSerAspAlaLysSerLeuLeu 377
DB 1546 ATCTTATGAGAGAGATTAAGATTTCCACGCACTTGTGCTCAGGAAACAAATCTCTTG 1605
QY 378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyProAspAspAlaLys 397
DB 1606 TCAGGTGTGCTGAAGAAAGATCTTAAGCAAAAGTTAGAGGGGCTCTGATGATGCCAAG 1665
QY 398 GluIleMetArgHiseSerPheSerGlyValaAsnTPGlnAspValTyrAspLysLys 417
DB 1666 GAGATTTAGCACACAAATTTCTTCTGCACTTGTGCTTGGCAAGATATCCGGAAGAG 1725
QY 418 LeuValProProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGlu 437
DB 1726 CTGTATACCTCATTTAAGCAACAATTACATCTGAACAAGATACAAAGATACCTTGATGA 1785
QY 438 GluPheThrAlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMet 457
DB 1786 GAATTTTACGACCAAGATGATTAACAATCACTCTCTGACCA-----GATACACGATG 1839
QY 458 AspCysMetAspAspGluArgArgProHisPheProGlnPheSerTyrSerAlaSerGly 477
DB 1840 GATGTGTAGCAATGAGAAAGACCTCATTTCTCAGTTCTCTTATTCACCCAGTGA 1899
RESULT 14
AD085348
ID AD085348 strand; cDNA; 2593 BP.
XX AD085348;
AC
XX
DT 07-OCT-2004 (first entry)

XX Human tumour-associated antigenic target (TAT) cDNA sequence #2162.
 DE human; tumour-associated antigenic target; TAT; cytosolic; gene therapy;
 KW cancer; cell proliferative disorder; gene; ss.
 XX Homo sapiens.
 OS
 PN MO2004060270-A2.
 XX
 PD 22-JUL-2004.
 XX
 PF 15-OCT-2003; 2003MO-US029126.
 XX
 PR 18-OCT-2002; 2002US-0418988P.
 XX
 PA (GENTH) GENENTECH INC.
 PA (MUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 PI Wu TD, Zhou Y;
 DR WPI; 2004-534300/51.
 PT
 PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
 PT preventing or treating cell proliferative disorders such as cancer.
 PS
 XX
 XX Claim 1; SEQ ID NO 2162; 5504bp; English.
 CC The present invention describes an isolated tumour-associated antigenic
 CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
 CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
 CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
 CC sequence identity to (a) - (c); or (e) a sequence that hybridises to (a) -
 CC (c). Also described: (1) an expression vector comprising the above
 CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
 CC a process for producing a polypeptide; (4) an isolated polypeptide
 CC comprising: (a) an amino acid sequence encoded by any of the above
 CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
 CC length coding region of the above nucleotide sequences; or (c) a sequence
 CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
 CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
 CC an isolated antibody that binds to the above polypeptide; (7) a process
 CC for producing the antibody; (8) an isolated oligopeptide that binds to
 CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
 CC binding organic molecule that binds to the above polypeptide; (10) a
 CC composition of matter comprising the above (chimeric) polypeptide,
 CC antibody, oligopeptide or TAT binding organic molecule, in combination
 CC with a carrier; (11) an article of manufacture comprising a container and
 CC the composition of matter contained within the container; (12) methods of
 CC inhibiting the growth of a cell that expresses the above protein, where
 CC the growth of the cell is at least in part dependent upon a growth
 CC potentiating effect of the above protein; (13) a method of
 CC therapeutically treating a mammal having a cancerous tumour comprising
 CC cells that express the above protein; (14) a method of determining the
 CC presence of a protein in a sample suspected of containing the protein
 CC described above; (15) methods of diagnosing the presence of a tumour in a
 CC mammal; (16) a method for treating or preventing a cell proliferative
 CC disorder associated with increased expression or activity of the above
 CC protein; and (17) a method of binding an antibody, oligopeptide or
 CC organic molecule to a cell that expresses the protein described above.
 CC The TAT sequences have cytosolic activities, and can be used in gene
 CC therapy. The composition and methods are useful for diagnosing,
 CC preventing or treating cancer. The composition is also used for preparing
 CC a medicament for the therapeutic treatment or diagnostic detection of a
 CC cell proliferative disorder or cancer. The present sequence represents a
 CC human TAT cDNA sequence from the present invention.
 XX
 SQ Sequence 2553 BP; 530 A; 747 C; 778 G; 538 T; 0 U; 0 Other;

Alignment Scores: 9.63e-211 Length: 2593
 Pred. No.: 2105.50 Matches: 397
 Score:

Percent Similarity: 90.21% Conservative: 36
 Best Local Similarity: 82.71% Mismatches: 42
 Query Match: 82.31% Indels: 5
 DB: 13 Gaps: 4
 US-09-869-079B-3 (1-479) x ADQ85348 (1-2593)

QY 1 MetSerAspValThrIleValysGluGlyTPValGlnIleArgGlyValGlyTyrIleIys 20
 DB 181 ATAGGAGCGTGGCTTGTGTGAAGAGGGTGGCTGCACAAAGAGGAGATCATCAAG 240
 QY 21 AsnTPArgProArgTyrPheLeuLeuIleThrAspGlySerPheIleGlyTyrIleGlu 40
 DB 241 ACCGSGCGGCGACGCTACTTCTCTCCCAAGAAATGATGACCTTCACTTGGCTCAAGAG 300
 QY 41 LysProGlnAspValAsp---LeuProTyrProLeuAsnAsnPheSerValAlaIysCys 59
 DB 301 CGGCGCGAGGATGTGACCAAGCGTAGGCTCCCTCAACAACTTCTGTGGCGCAGTGC 360
 QY 60 GlnLeuMetIleThrGluArgProIleProIleThrPheIleIleArgCysLeuGlnIleTP 79
 DB 361 CAGCTGATGAGAGCGAGCGGCGCCCGCCCAACACCTTATCATCTCGCTGCGCAGTGG 420
 QY 80 ThrThrValIleGluArgThrPheHisValAspThrProGluGluArgGluIleTPThr 99
 DB 421 ACCACTGTATGACGACGACCTTCCATGTGAGACTCTCTGAGAGCGGAGAGATGAGAC 480
 QY 100 GluAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCys 119
 DB 481 ACCGCCATCAAGACTGTGGCTGACCGGCTCAAGAAACAGAGAGAGATGAGATCTTC 540
 QY 120 SerProThrSerGlnIleAspAsnIleGlyGluGluIleMetAspAlaSerThrThrHis 139
 DB 541 CGGTGGGCTCACCCAGTACAACTCAGGCGCTGAAGAGATGAGATGTCCTGCGCAAG 600
 QY 140 HisIys---ArgIleThrMetAsnAspPheAspTyrLeuIleLeuGluGlyIysGlyTyr 158
 DB 601 CCCAGACACCGCTGACCTGACATGAAACAGATTGACTTGAAGCTCTGGGCAAGGCACT 660
 QY 159 PheGlyIysValIleLeuValArgIleValAspGlyIysAspTyrIleValMetIysIle 178
 DB 661 TTGGCAAGAGTATCTGTGTGAAGAGGACAGGCGCGCTACTACCAAGCATGAAGATC 720
 QY 179 LeuIleValGluValIleIleAlaIleValAspGluValAlaHisThrIleThrGluSerArg 198
 DB 721 CTCMAAGAGAGTCTCTGTGGCAAGAGCGAGTGGCCACACACTCCAGGAACCCG 780
 QY 199 ValLeuIleAsnThrArgHisAspProPheLeuThrSerLeuIleTyrSerPheGlnThrIys 218
 DB 781 GTCTTCAGAACTCCAGGACCCCTTCTCAAGCCCTTAAGTACTCTTCCAGACCCAC 840
 QY 219 AspArgLeuCysPheValMetGluTyrValAsnGlyIleGluLeuPhePheHisLeuSer 238
 DB 841 GACCGCTCTGCTTGTTCATGAGATCGCCACAGGGGCGAGCTGTCTTCCACCTGCTCC 900
 QY 239 ArgGluArgValPheSerGluAspArgThrArgPheTyrGlyValAspIleValSerAla 258
 DB 901 CGGAAACGCTGTCTCCAGAGACCGCGGCCCGCTTCAAGGCGCTAAGATTGTGAGCC 960
 QY 259 LeuAspTyrLeuHisSerGlyIys---IleValTyrArgAspLeuIleGluAsnLeu 277
 DB 961 CTGATTAATCTGACCTCGAGAGAAAGACGTGGTGTACCGGACCTCAAGCTGAGAACTC 1020
 QY 278 MetLeuAspLysAspGlyIleIleValIleThrAspPheGlyLeuCysIleGluGlyIle 297
 DB 1021 ATGCTGACAAAGACCGGACATTAAGATCAAGACTTGGGCTGTGCAAGAGGGGAGATC 1080
 QY 298 ThrAspAlaAlaThrMetIleThrPheCysGlyThrProGluTyrLeuAlaProGluVal 317
 DB 1081 AAGGACGGTGCACCACTGAAGACCTTTTGGCAGACCTGAGATGACTGGCCCCCGAGG 1140
 QY 318 LeuGluAspAsnAspTyrGlyArgAlaValAspTyrIleGluGlyValIleMetTyr 337

Db 1141 CTGAGACAAATGACTACGCGCTGCGATGAGACTGTGGGGGCTGGGCTGTCATGTAC 1200
QY 338 GJUMETMetCygllyrgrleupProPheTyraAnglAAspHisGluLysLeuPheGluLeu 357
Db 1201 GAGATGATGAGCGCTGCTGCTTCTCAACACAGACACATGAGAGCTTTTGTAGCTC 1260
QY 358 ILeuMeGluAAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377
Db 1261 ATCTCATGAGAGATCCGCTTCCCGCGACGCTTGTCGCCAGGCCAAGTCTTGCTT 1320
QY 378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyProAspAspAlaLys 397
Db 1321 TCAGGCTCTCTCAAGAGAGACCCCAAGCAGAGCTTGCGGGGCTGCCAAGACGCGCAAG 1380
QY 398 GJUMETMetArgHisSerPhePheSerGlyValAsnThrGlaAspAlaTyraAspLysLys 417
Db 1381 GAGATATGATGATGATGCTTCTTGCGGATGTGTGTGGACAGCTGTACGAGAAAGAG 1440
QY 418 LeuValProProPheLysProGlnValThrSerGluThrAspThrArgTyraPheAspGlu 437
Db 1441 CTCAGCCCAACCTTCAAGCCCAAGCCGTCAGTGGAGACCTGACACCGATATTTTGTAG 1500
QY 438 GluPheThrAlaGlnThrIleThrIleThrProProGluLysTyraAspGluAspGlyMet 457
Db 1501 GAGTTCACGCGCCAGATGATGATCAACACACACACCTGACCAA-----GATGACACCATG 1554
QY 458 AspCysMetAspAsnGluArgProHisAspPheProGluPheSerTyraSerLysArgLys 477
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RESULT 15
ACD44893
ID ACD44893 standard; cDNA; 2978 BP.
AC ACD44893;
XX
XX 10-SEP-2003 (first entry)
DE Human signal transduction pathway component HJBCK80 cDNA.
XX
XX Human; signal transduction pathway component; gene; ss; gene therapy;
XX neural disorder; immune system disorder; systemic lupus erythematosus;
XX rheumatoid arthritis; multiple sclerosis; muscular disorder; sinusitis;
XX respiratory disease; nasal vestibulitis; nasal polyp; pulmonary disorder;
XX cardiovascular disorder; congenital heart defect; Epstein's anomaly;
XX hypoplastic left heart syndrome; renal disorder; acute kidney failure;
XX end-stage renal disease; hyperproliferative disorder; Hodgkin's disease;
XX leukemia; inflammatory disease; septic shock; buritis; appendicitis;
XX allergy; asthma; blood related disorder; thrombosis; atherosclerosis;
XX myocardial infarction; endocrine disorder; Addison's disease; dysphagia;
XX corticosteroid deficiency; reproductive system disorder; dysmenorrhea;
XX testicular atrophy; gastrointestinal disorder; irritable bowel syndrome;
XX infectious disease; cancer; wound healing; epithelial cell proliferation.
XX
OS Homo sapiens;
XX
XX US2003036505-A1.
XX
XX 20-FEB-2003.
XX
XX 20-SEP-2001; 2001US-00955999.
XX
XX 25-SEP-2000; 2000US-0234997P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Barash SC, Ni J, Ruben SM, Rosen CA, Young PE, Rohrschneider LR;
XX
XX MPI; 2003-492122/46.
XX
XX P-PSDB; ABO27207.
XX
XX New isolated nucleic acids encoding signal transduction pathway component
XX PT polypeptides, useful for diagnosing, treating, and/or preventing

PT disorders, such as cancer, infections, cardiovascular and inflammatory
PT diseases.
XX
XX Claim 3; Page 224-226; 297pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule. The methods
XX and compositions of the present invention are useful for diagnosing,
XX treating, preventing and/or prognosing disorders related to the novel
XX polypeptides, such as neural disorders, immune system disorders (e.g.
XX systemic lupus erythematosus, rheumatoid arthritis, or multiple
XX sclerosis), muscular disorders, respiratory diseases (e.g. nasal
XX vestibulitis, nasal polyps, or sinusitis), reproductive disorders,
XX gastrointestinal disorders, pulmonary disorders, cardiovascular disorders
XX (e.g. congenital heart defects, Epstein's anomaly or hypoplastic left
XX heart syndrome), renal disorders (e.g. acute kidney failure, or end-stage
XX renal disease), hyperproliferative disorders (e.g. Hodgkin's disease or
XX leukemia), inflammatory diseases (e.g. septic shock, buritis, or
XX appendicitis), allergic reactions and conditions (e.g. asthma), blood
XX related disorders (e.g. thrombosis, atherosclerosis or myocardial
XX infarction), endocrine disorders (e.g. Addison's disease or
XX corticosteroid deficiency), reproductive system disorders (e.g.
XX testicular atrophy or dysmenorrhea), gastrointestinal disorders (e.g.
XX dysphagia or irritable bowel syndrome), infectious diseases, and/or
XX cancerous diseases. The polynucleotides can also be used to aid wound
XX healing and epithelial cell proliferation. The present sequence
XX represents a human signal transduction pathway component cDNA

Sequence 2978 BP; 613 A; 842 C; 889 G; 627 T; 0 U; 7 Other;
SQ

Alignment Scores:
Pred. No.: 1,166-210 Length: 2978
Score: 2105.50 Matches: 397
Percent Similarity: 90.21% Conservative: 36
Best Local Similarity: 82.71% Mismatches: 42
Query Match: 82.31% Indels: 5
DB: Gaps: 4

US-09-869-079B-3 (1-479) x ACD44893 (1-2978)

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Db 551 ACTGCGCGCCACGCTACTTCTCTCAAGATGATGACACTTCAATGGCTCAACAAGAG 610
QY 41 LysProGlnAspValAsp---LeuProTyraProLeuAsnAsnPheSerValAlaLysCys 59
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QY 60 GlnLeuMetLysThrGluArgProLysProAsnThrPheIleLysCysLeuGlnTTP 79
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Db 791 ACCGCCATCAGACTGTGGCTGACGCGCTCAAGAAGACAGAGAGAGATGACTTC 850
QY 120 SerProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrHis 139
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QY 140 HisLys---ArgLysThrMetAsnAspPheAspTyraLeuLysLeuGluLysGlyThr 158
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Search completed: April 13, 2005, 09:07:38
Job time : 675 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 13, 2005, 07:36:25 ; Search time 236 Seconds
(without alignments)
3321.087 Million cell updates/sec

Title: US-09-869-079B-3

Perfect score: 2558
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2558	100.0	1547	4	US-09-851-670-1	Sequence 1, Appl1
2	2100.5	82.1	2626	4	US-09-590-740-5	Sequence 5, Appl1
3	2099.5	82.1	2181	4	US-09-417-197-70	Sequence 138, Appl1
4	2099.5	82.1	2184	4	US-09-417-197-138	Sequence 1, Appl1
5	2099.5	82.1	2610	2	US-09-212-771-1	Sequence 1, Appl1
6	2099.5	82.1	2610	3	US-09-081-058-1	Sequence 1206, Ap
7	2099.5	82.1	2610	4	US-09-023-655-1206	Sequence 1, Appl1
8	2099.5	82.1	2610	4	US-09-590-740-1	Sequence 1, Appl1
9	2004	78.3	1599	3	US-09-256-465-1	Sequence 3, Appl1
10	2004	78.3	1599	3	US-09-167-322-3	Sequence 1004, Ap
11	2004	78.3	1599	4	US-09-023-655-1004	Sequence 3, Appl1
12	1798.5	70.3	1254	4	US-09-590-740-3	

13	916	35.8	1338	4	US-10-067-977-1	Sequence 1, Appl1
14	909	35.5	2370	3	US-09-031-295-1	Sequence 1, Appl1
15	905	35.4	2311	2	US-08-712-709-6	Sequence 6, Appl1
16	905	35.4	2311	3	US-09-111-444-6	Sequence 6, Appl1
17	905	35.4	2311	3	US-09-541-228-6	Sequence 772, Appl1
18	905	35.4	2311	4	US-09-016-434-772	Sequence 1676, Ap
19	872	34.1	2239	4	US-09-949-016-1676	Sequence 3, Appl1
20	865	33.8	2274	4	US-09-772-647-3	Sequence 1735, Appl
21	849	33.2	2336	4	US-09-949-016-1735	Sequence 1, Appl1
22	838	32.8	2599	6	5266464-1	Patent No. 5266464
23	838	32.8	2599	6	5266464-1	Patent No. 5266464
24	834.5	32.6	3321	4	US-09-023-655-1361	Sequence 1361, Ap
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26	829	32.4	2245	3	US-09-225-749-24	Sequence 24, Appl1
27	823.5	32.2	2196	1	US-08-313-274-1	Sequence 1, Appl1
28	823.5	32.2	2262	4	US-09-949-016-5805	Sequence 5805, Ap
29	821.5	32.1	2751	4	US-09-417-197-72	Sequence 72, Appl1
30	819.5	32.0	3255	4	US-09-016-434-1471	Sequence 1471, Ap
31	819.5	32.0	6102	4	US-09-949-016-2007	Sequence 2007, Ap
32	807	31.5	2127	4	US-09-270-767-13509	Sequence 13509, A
33	807	31.5	2244	3	US-09-094-714A-48	Sequence 48, Appl1
34	798.5	31.2	2968	4	US-08-685-852-1	Sequence 1, Appl1
35	796	31.1	2705	4	US-09-949-016-839	Sequence 839, App
36	796	31.1	2715	4	US-09-949-016-1959	Sequence 1959, App
37	791.5	30.9	1636	4	US-09-016-434-1433	Sequence 1433, Ap
38	789.5	30.9	2506	4	US-09-949-016-1475	Sequence 1475, Ap
39	786	30.7	2754	3	US-09-429-322-3	Sequence 3, Appl1
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43	781.5	30.6	2201	4	US-09-566-921-52	Sequence 52, Appl1
44	769.5	30.1	1413	4	US-09-248-796A-4379	Sequence 4379, Ap
45	766.5	30.0	2499	4	US-09-949-016-5704	Sequence 5704, Ap

ALIGNMENTS

RESULT 1
US-09-851-670-1
; Sequence 1, Application US/09851670
; Patent No. 6809194
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; TITLE OF INVENTION: AKT3 INHIBITORS
; FILE REFERENCE: PP-01699.002/200130.520
; CURRENT APPLICATION NUMBER: US/09/851,670
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-851-670-1
US-09-869-079B-3 (1-479) x US-09-851-670-1 (1-1547)
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Score: 2558.00
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Length: 1547
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Conservative: 0
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; Sequence 5, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2626
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-590-740-5

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Query Match: 82.11% Indels: 5
DB: 4 Gaps: 4

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DB 344 ACCTGCGCGCACGCTACTCTCTCTCAAGAACATGAGACCTTTATTTGGCTTACAAAGAA 403
QY 41 LysProGlnAspValAsp---LeuProTyTrProLeuAsnAsnPheserValAlaLysCys 59
DB 404 CCGCTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 463
QY 60 GlnLeuMetLysThrGluArgProLysProAsnThrPheIleArgCysLeuGlnTrp 79
DB 464 CAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 523
QY 80 ThrThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTrpThr 99
DB 524 ACCAAGTCATTTGAGCGACCTTCCATGATGAGAAAGCTGAGAGAGAGAGAGAGAGAGAG 583
QY 100 GluAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCys 119
DB 584 ACCGCTTACAGACTGTGCGCATGATGATGATGATGATGATGATGATGATGATGATGATG 643
QY 120 SerProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrHis 139
DB 644 CGATCAGGCTCACCCAGTGAACAATCAGGAGGCTGAAGATGATGATGATGATGATGATG 703

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QY 219 AsparGLeuCySphValMetGluTyValAsnGlyGlyGluLeuPhePheHisLeuSer 238
    |||||
Db 661 GACCGCTCTGCTTTTCATGAGTACGCCAAGGGGGAGGTGTTCTTCCACCTGTCC 720

QY 239 ArgGluArgValPheSerGluAspArgThrArgPheTyGlyAlaGluIleValSerAla 258
    |||||
Db 721 CGGGAACGTGTGTTCTCCAGAGACCGGCGCGCTTATGCGCTGAGATTGTGTACGCC 780

QY 259 LeuAspTyLeuHisSerGlyLys---IleValTyArgAspLeuLysLeuGluValLeu 277
    |||||
Db 781 CTGACTACTGCTGACCTCGAGAGAAAGTGTGTACCGGAGCTCAAGCTGAGAAACCTC 840

QY 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCySphGlyGlyIle 297
    |||||
Db 841 ATGCTGACAGAGACGGGACATTAGATACAGACTTGGGCTGTGCAAGAGGGAGATC 900

QY 298 ThrAspAlaAlaThrMetLysThrPheCySglYThrProGluTyLeuAlaProGluVal 317
    |||||
Db 901 AAGGACGTGCGCCACATGAAAGACCTTTGCGGACACCTGAGTACCTGCGCCCGAGGTG 960

QY 318 LeuGluAspAspAspTyGlyArgAlaValAspTrpGlyLeuGlyValValMetTyTr 337
    |||||
Db 961 CTGGAGAGACATGACTACGGCGGTGCACTGAGTGTGGGCTGGGCTGTGTCATGTAC 1020

QY 338 GluMetMetCySglYArgLeuProPheTyAsnGluAspHisGlyLysLeuPheGluLeu 357
    |||||
Db 1021 GAGATGATGTGGGTGCGCTGCGCTTCTTCAACACAGACCATGAGAACTTTTGTAGCTC 1080

QY 358 IleLeuMetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377
    |||||
Db 1081 ATCCCTCATGAGAGATCCGCTTCCGCGCACCGCTTGTCCCGAGGCCAAGCTCTGTGCTT 1140

QY 378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyIleProAspAspAlaLys 397
    |||||
Db 1141 TCGGGCTGCTCAAGAAAGACCCCAAGGCTTGGGGGGCTCCGAGAGCGCAAG 1200

QY 398 GluIleMetArgHisSerPhePheSerGlyValAsnTrpGluAspValTyArgLysLys 417
    |||||
Db 1201 GAGATCATGACAGATGCTTCTTTCGCGGTATGTGTGGCAGACGCTGTACAGAAAGAG 1260

QY 418 LeuValProProPheLysProGluValThrSerGluThrAspThrArgTyTrPheAspGlu 437
    |||||
Db 1261 CTCAGGCCACCTTCAAGGCCCGGCTGACGTCCGAGACGTACACCGGTATTTGTATGAG 1320

QY 438 GluPheThrAlaGlnThrIleThrIleThrProProGluLysTyArgAspGluAspGlyMet 457
    |||||
Db 1321 GAGTTACGGCCCGAGATGATCACCATCACCACTGACCA-----GATGACAGCATG 1374

QY 458 AspCyMetAspAsnGluArgArgProHisPheProGluPheSerTySerAlaSer 476
    |||||
Db 1375 GAGTGTGTGACAGAGGAGCGGCGCCCACTTCCCACTTCTCCACTCGGCGACG 1431

RESULT 4
US-09-417-197-138
; Sequence 138, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Oie THASTRUP, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 138
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EGFP-PKB fusion
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (1)..(2181)
US-09-417-197-138

Alignment Scores:
Pred. No.: 5,11e-236 Length: 2184
Score: 2099.50 Matches: 396
Percent Similarity: 90.19% Conservative: 36
Best Local Similarity: 82.67% Mismatches: 42
Query Match: 82.08% Indels: 5
DB: Gaps: 4

US-09-869-079b-3 (1-479) x US-09-417-197-138 (1-2184)

QY 1 MetSerAspValThrIleValLysGluGlyTrpValGlnLysArgGlyGluTyTrIleLys 20
    |||||
Db 742 ATGAGCGAGTGGCTATTGTGTGAAAGAGGTGGCTGCAAAACGAGGAGATCATCAG 801

QY 21 AsnTrpArgProArgTyTrPheLeuLeuLysThrAspGlySerPheIleGlyTyTrLysGlu 40
    |||||
Db 802 ACCTGCGCGCCACGCTACTTCTCTCTCAAGATGATGACCTTCAATTGGCTACAGAGG 861

QY 41 LysProGluAspValAsp---LeuProTyProLeuAsnAsnPheSerValAlaLysCys 59
    |||||
Db 862 CGCGCGCAGAGATGTGACCAACGTGAGGCTCCCTCCCAACACTTCTGTGTGCGCAGTGC 921

QY 60 GluLeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCySphGlnTrp 79
    |||||
Db 922 CAGCTGATGAAACGAGAGCGGCGCGCCCAACCTTCAATCATATCCGCTGCGAGTGG 981

QY 80 ThrThrValIleGluArgThrPheHisValAspThrProGluGluArgGluTrpThr 99
    |||||
Db 982 ACCACTGTCATGACGACGACCTTCCATGTGAGACTCTCTGAGAGACGGAGAGTGCACA 1041

QY 100 GluAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetLysCys 119
    |||||
Db 1042 ACCGCCATCCACACTGTGTGCTGACGCGCTCAAGAGCAGAGAGAGAGAGATGACCTTC 1101

QY 120 SerProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrHis 139
    |||||
Db 1102 CGGTGGGCTACCCAGTGCACACTCAGGGGCTGAAGAGATGAGAGTGTCTCTGCGCAG 1161

QY 140 HisLys---ArgLysThrMetAsnAspPheAspTyTrLeuLysLeuGlyLysGlyThr 158
    |||||
Db 1162 CCCAAGCACCGCGGTACCATGACGATTGTGATCTCTGAGCTGCTGCGGACAGGCACT 1221

QY 159 PheGlyLysValIleLeuValArgGluLysAlaSerGlyLysTyTrAlaMetLysIle 178
    |||||
Db 1222 TTCGGCAAGGTGATCTGGGTGAAGAGAGGCAAGGCCGCTTACTTACGCCATGAAATC 1281

QY 179 LeuLysLysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArg 198
    |||||
Db 1282 CTCAGAAAGAGATGATGTGTGCCAAGACGAGGTGGCCACACACTCACCGAAGACGC 1341

QY 199 ValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTyTrSerPheGlnThrLys 218
    |||||
Db 1342 GTCCTGCAAGACTCCAGGACACCTTCTCTCAAGCCCTGAGATCTCTTCCAGACCCAC 1401

QY 219 AsparGLeuCySphValMetGluTyValAsnGlyGlyGluLeuPhePheHisLeuSer 238
    |||||
Db 1402 GACCGCTCTGCTTTGTGTATGAGTACGCCAAGGGGGAGAGCTTCTTCCACCTGTCC 1461

QY 239 ArgGluArgValPheSerGluAspArgThrArgPheTyGlyAlaGluIleValSerAla 258
    |||||
Db 1462 CGGGAACGTGTGTTCTCCAGAGACCGGCGCGCTTATGCGCTGAGATTGTGTACAGC 1521

QY 259 LeuAspTyLeuHisSerGlyLys---IleValTyArgAspLeuLysLeuGluValLeu 277
    |||||
Db 1522 CTGGACTACTGCTGCTCGAGAGAAAGTGTGTACCGGAGCTCACTGAGAGAACTCTC 1581

QY 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCySphGlyGlyIle 297
    |||||
Db 1582 ATGCTGACAGAGAGCGGACATTAAAGATCACAGACTTGGGCTGTGCAAGAGCGGAGATC 1641

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Qy 298 ThrAspAlaIaThrMetLysThrPheCysGlyThrProGluTrpLeuAlaProGluVal 317
Db 1642 AAGGACGGTGCACCAAGAAAGACCTTTGGCGCACACCTGAGTACCTGGCCCCGAGAGTG 1701
Qy 318 LeuGluAspAsnAspTrpGlyArgAlaValAspTrpGlyLeuGlyValAlaMetTyr 337
Db 1702 CTGAGGACCAATGACTACCGCGCGTGCAGTGCAGTGGGGCTGGGGCTGGTCACTATC 1761
Qy 338 GluMetCysGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGluLeu 357
Db 1762 GAGATGATGTCGGTCCCTGCTTCTTACACAGACCATGAGAGCTTTTGAAGCTC 1821
Qy 358 IleuMetCysGluAspIleuLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377
Db 1822 ATCTCATGAGAGGATCCCTTCCCGCACGCTTGCTCCGAGGCAAGCTTCTGCTT 1881
Qy 378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyProAspAspAlaLys 397
Db 1882 TCAGGCGTCTCAAGAAAGAACCCCAAGACAGCTTGGCGGGCTCCGAGAGCCCAAG 1941
Qy 398 GluIleMetArgHisSerPhePheSerGlyValAsnTrpGlnAspValTyrAspLysLys 417
Db 1942 GAGATCATGACGACCTCTTGGCGGATCGTGGCAGCAGTGTACGAGAAAGAG 2001
Qy 418 LeuValProProPheLysProGlnValThrSerGluThrAspTrpArgTyrPheAspGlu 437
Db 2002 CTGAGCCACCTTCAAGCCCGAGTCACTGAGCTGAGCTGACACAGATTTTGTAGAG 2061
Qy 438 GluPheThrAlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMet 457
Db 2062 GAGTTCAGCGCCAGATGATCACCATCACACACCTACCA-----GATGACAGCATG 2115
Qy 458 AspCysMetAspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSer 476
Db 2116 GAGGTGTGACAGACGAGCGACGCGCCACTTCCCGAGTTCTCTACGCGCAGC 2172

RESULT 5

US-09-212-771-1
; Sequence 1, Application US/09212771
; Patent No. 5958773
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
; FILE REFERENCE: RTS-0034
; CURRENT APPLICATION NUMBER: US/09/212, 771
; CURRENT FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1641)
US-09-212-771-1

Alignment Scores:

Pred. No.:	6,736-236	Length:	2610
Score:	2099.50	Matches:	396
Percent Similarity:	90.19%	Conservative:	36
Best Local Similarity:	82.67%	Mismatches:	42
Query Match:	82.08%	Indels:	5
DB:	2	Gaps:	4

US-09-869-079b-3 (1-479) x US-09-212-771-1 (1-2610)

Qy 1 MetSerAspValThrIleValLysGluGlyTrpValAlaLysArgGlyLysIleLys 20
Db 199 ATGGGACCGTGGCTATTTGAGAGAGGAGGTTGGCTGCACAAACGAGGGAGTACATCAAG 258
Qy 21 AsnTrpArgProArgTyrPheLeuLeuLysThrAspLysSerPheIleGlyTyrLysGlu 40

Db 259 ACCGCGGCGGACGCTACCTTCTCTCAAGAAAGATGACACCTTACCTGGCTCAAGAG 318
Qy 41 LysProGlnAspValAsp---LeuProTyrProLeuAsnAsnPheSerValAlaLysCys 59
Db 319 CGGCCCCAGGATGTGACCAACGTGAGGCTCCCTCAACAACCTTCTGTGGCGGAGTGC 378
Qy 60 GluLeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTrp 79
Db 379 CAGCTATGAAAGCGAGCGGCGCCCGCCCAACCTTCACTCACTCCGCTGCGCAGTGG 438
Qy 80 ThrThrValIleGluArgThrPheHisValAspThrProGluGluArgGluTrpTrp 99
Db 439 ACCACTGTCACTCAAGCCACTTTCATGTGAGACTCTCTGAGAGCGGAGAGGTGAGCA 498
Qy 499 ACCGCGATCCAGACTGTGGCTGACGCGCTCAAGAACAGAGAGGAGAGAGTTC 558
Db 120 SerProThrSerGlnIleAspAsnIleGlyGluGluMetCysAspAlaSerThrTrpHis 139
Qy 559 CGGTGGGCTCACCCAGTGCACATCAGGGGCTGAAGAGATGAGGTGCTCCGCGCAAG 618
Db 140 HisLys---ArgLysThrMetAspAspPheAspTyrLeuLysLeuGlyLysGlyThr 158
Qy 619 CCAGAGCAGCGGTGACCATGAACAGATTGAGTACTTGAAGCTGTGGGCAAGGCACT 678
Qy 159 PheGlyLysValIleLeuValArgLysLysValAspGlyLysTyrTrpAlaMetLysIle 178
Db 679 TTGGGCAAGGTATCTCTGTGAAGAGAGGAGGAGGCGGCTACTACGCATGAGATG 728
Qy 179 LeuLysLysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArg 198
Db 739 CTCMAAGAGAACTCATCTGTGGCAAGAGAGAGAGTGGCCACATCCACCGAAGCCCG 798
Qy 199 ValLeuLysAsnThrArgHisAspProPheLeuThrSerLeuLysTyrSerPheGlnTrpLys 218
Db 799 GTCTTCGAGACTCCAGGACCCCTTCTCAAGCCCTGAAGTACTTTCGAGACCCAC 858
Qy 219 AspArgLeuCysAspValMetGluTrpValAsnGlyGlyLeuPhePheHisLeuSer 238
Db 859 GACCGCTCTGCTTGTTCATGAGGTACGCCAAGGAGGAGGAGTGTCTTCCACCTGTC 918
Qy 239 ArgGluArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAla 258
Db 919 CGGGAACGTGTCTCCAGAGACCGCGGCTTCTATGAGGCTGAGATGTGTGACCC 978
Qy 259 LeuAspTyrLeuHisSerGlyLys---IleValTyrArgAspLeuLysLeuGluAsnLeu 277
Db 979 CTGGACTACCTGCACTCGAGAGAGACGTGGTGTACCGGACCTCAAGCTCGAGAACCTC 1038
Qy 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIle 297
Db 1039 ATGCTGACAAAGAGCGGACATTTAGATCAACAGACTTGGGGTGTGCAAGAGGGAGATC 1098
Qy 298 ThrAspAlaIaThrMetLysThrPheCysGlyThrProGluTrpLeuAlaProGluVal 317
Db 1099 AAGGACGGTGCACCACTGAAGACCTTTGCGGACACTGAGTACCTGCGCCCCGAGAGTG 1158
Qy 318 LeuGluAspAsnAspTrpGlyArgAlaValAspTrpTrpGlyLeuGlyValAlaMetTyr 337
Db 1159 CTGAGAGCAATGACTACGCGCGTGCAGTGTGAGTGGGGCTGGGCTGGTCACTATGC 1218
Qy 338 GluMetMetCysGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGluLeu 357
Db 1219 GAGATGATGTGGGTGCTGCTGCTTCTTCAACAGAGACATGAGAGAGCTTTTGTAGCTC 1278
Qy 358 IleuMetCysGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377
Db 1279 ATCTCATGAGAGATCCGCTTCCCGCAGCGCTTGTCCGAGGCGCAAGTCTTGTGCTT 1338
Qy 378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyProAspAspAlaLys 397

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Db      1339 UCAGGGCTGCTCAGAAAGAACCCCAAGAGAGAGCTTGGCGGGGGGCTCCGAGAGAGCCAAg 1338
QY      398 GIUIlMeArGhiSeSerPhePheSeSerGIyValAntYpGlnAspValTYrAspLysIys 417
Db      1399 GAGATCATGACGATCGGCTTCTTTTCCCGGTATCGGTGGAGACAGCTGTACGAAAGAAg 1458
QY      418 LeuValProProPheLysProGlnValPheSeSerGlnUmTrpAspThrArgTYrPheAspGlu 437
Db      1459 CTCAGCCCAACCTTCAAGCCCCAGGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1518
QY      438 GluPheThrAlaGlnThrIleThrIleThrProProGluLysTYrAspGluAspLysMet 457
Db      1519 GAGTTCACAGCGCCGACGATGATCATCATCATCACCACTGACCA-----GATGACAGCATG 1572
QY      458 AspCysMetAspAsnGluArgArgProHisPheProGlnIlePheSerTYrSerAlaSer 476
Db      1573 GAGTGTGTGACAGAGCAGCAGCAGCGCCACCTTCCCGCAGTTCTCTTACTCGGCGCAGC 1629

RESULT 6
US-09-091-058-1
; Sequence 1, Application US/09091058
; Patent No. 6054285
; GENERAL INFORMATION:
; APPLICANT: Hemmings, Brian A.
; APPLICANT: Frech, Mathias
; TITLE OF INVENTION: Screening Method
; FILE REFERENCE: 4-20683/A/20684/PCT
; CURRENT APPLICATION NUMBER: US/09/091_058
; CURRENT FILING DATE: 1998-06-10
; EARLIER APPLICATION NUMBER: PCT/EP96/04814
; EARLIER FILING DATE: 1996-11-05
; EARLIER APPLICATION NUMBER: 9525703.6
; EARLIER FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1641)
US-09-091-058-1

Alignment Scores:
Pred. No.:      6,73e-236      Length:      2610
Score:          2099.50      Matches:      396
Percent Similarity: 90.19%      Conservative: 36
Best Local Similarity: 82.67%      Mismatches: 42
Query Match:      82.08%      Indels:      5
DB:              3      Gaps:      4

US-09-869-079B-3 (1-479) x US-09-091-058-1 (1-2610)
QY      1 MeSeSerAspValThrIleValIysGlnGlyTYrValGlnLysArgGlyGlnTYrIleLys 20
Db      199 ATGACGCGACGTGGCTATTGTGAAGAGAGGTGGCTGCACAAACGAGGAGAGTACATCAAG 258
QY      21 AsnTrpArgProArgTYrPheLeuLeuLysThrAspGlySerPheIleGlyTYrIlyGlu 40
Db      259 ACCTGGCGGCGCACGGTACTCTCTCTCAAGATGATGGCACCTTCATTGGCTACAAAGAG 318
QY      41 LysPProGlnAspValAsp---LeuProTYrProLeuAsnAsnPheSerValAlaLysCys 59
Db      319 CGGCGCGCAGAGTGTGGACCAACGTAGAGCTCCCTCAACAACTTCTCTGTGGCGCAGTGC 378
QY      60 GlnLeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTrp 79
Db      379 CAGCTGATGAGAGCGAGGAGGCGCGGCGCAACACTTCATCATCTCGTGGCTGAGTGG 438
QY      80 ThrThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTrpThr 99
Db      439 ACCACTGTATCATCGAAGCGACCTTCATGTGAGACCTCTCTGAGCGAGCGGAGAGTGTGACA 498

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QY	100	GLUHLALIEGGLNALVALNALAASPAARGLEUHLNARGIINGIUGIUGIWAHMEASACYS	113
Db	499	ACCGCATTCACAGACTGTGGCTGAAGGCCCTCAAGAGACGAGAGAGAGATGAACTTC	558
QY	120	SEPRPOTHSESGIINLEASPAASNIIGLYGUUGIUGIUMETASPAALASERTHTRHIS	139
Db	559	CGGTCCGGGCTACCCAGTGNACAACTCAAGGGGCTGAAGAGATGAGAGTCTCCGGCCAA	618
QY	140	HISLYS--ARGLYSTHMETASNPASNPHEASPTYRLEUYSLEULEUGIYLYSGLYTHR	158
Db	619	CCCAAGACACCCCGTAGCCATGAAAGAGATTGAAGTCACTGAAGCTGCTGGGCAAGGGCACT	678
QY	159	PHEGIYLYSVALLILEUVALARGIULYALASERGILYVSTYRTRALAMETLYILE	178
Db	679	TTCCGCAAGGAGATCTCGTGTAAGAGAGAGGCCACAGGCCCTACTACAGCCATTAAGATC	738
QY	179	LEUYSLYSGIULVALILELEALALYSASPGLUVALAHISTHTRLEUTHGUSERARG	198
Db	739	CTCAAGAAAGAAAGTCATCTGTGGCCAAAGAGAGAGTGGCCCACTCACTCAACGNAACGC	798
QY	199	VALLEUYSANTRHARGHISPRPHELEUTHISERLEUYSYRYSERPHEGINTHLYS	218
Db	799	GTCTCGCAGAACTCGAGGCAACCCCTTCTCAACAGCCTGAAGTACTCTTTCCACAAACCAC	858
QY	219	ASPARTRGUCYSPHEVALMETGINTYRVALASNIIGLYGILEUPEPHEHISLEUSER	238
Db	859	GACCGCCTCTCTTGTCATGAGATGACCAACAGGGAGAGACTGTTCTTCCACTCTGCC	918
QY	239	ARGGLIARVALPHESERGILUASPARGTTHRARGPHERYRGILAGIULIEVALISERALA	258
Db	919	CGGGAAGGTGTGTTCTCCGAGACCGGGCCCGCTTATGGCGCTGAGATTGTGTGACCC	978
QY	259	LEUASPTYRLEUHIASERGILYLYS---ILEVALYRARGASPLEUYSLEUGIUAANLEU	277
Db	979	CTGACATCACCTGCACCTCGAGAAACAGTGGTGTGACCGGACCTTCAAGCTGGAAACCTC	1038
QY	278	METLEUASPLYSASPGIYHISILELYSIIETHRASPHEGIYLEUCYSLYSGLUGIYILE	297
Db	1039	ATCTCGACAAAGACGGGCACATTAAAGATCACAGACTTCGGGCTGTGCAGAGAGGGATC	1098
QY	298	THRASPAALATHRMETLYSTHPRHESYSGIYTHRPROGIUTYRLEUALAPROGIUVAL	317
Db	1099	AAGAGCGGTGCCACCATGAAAGACCTTTTGGCGGACACTGAGTACGTGGCCCGCAAGTGT	1158
QY	318	LEUGIUSPASPANASPTYRGLYARGALAVALLASPTTPTRPGIYLEUGIYVALIMETCYR	337
Db	1159	CTGGAGGACATGACTACAGGCCCGGAGTGACTGTGGGGGCTGGGCGTGGTCAATGTAC	1218
QY	338	GLUMETMETCYSGIYARGLEUPRPHETRYRANGINASPHISGILULYSLEUPHEGIULEU	357
Db	1219	GAGATGATGTCCGGTCCGCTCCCTCTTACACAGACCAATGAGAAAGCTTTTGAAGCTC	1278
QY	358	ILELEUNETGIUASPIELIYSPHESPROARGTTHRLEUSERASPAALALYSSEULEUEN	377
Db	1279	ATCTCATGAGAGAGATCCGCTTCCCGGCGACGCTTGCTCCGAGCCAAAGTCTTCTCTT	1338
QY	378	SERGIYLEULEUILLIYASPRPROASMLYARGILEUGIYGLIYPRORASPAALALYS	397
Db	1339	TCAGGGCTGCTCAAGAAAGACCCCAACAGAGGCTTGGCGGGGCTCCGAGAGAGCCAAAG	1398
QY	398	GLIULIEMETARGHISERPHESERSEGIYVALIANTPRGLINASPVALLYRASPILYSLE	417
Db	1399	GAGATCATGACGACATCGCTTTTGGCCGGTACTGTGGCGACGACGCTGACGAADAAGAG	1458
QY	418	LEUVALPROROPHELYSPROGINVALIATHSERGIUTHRASPTHRARGYRPHASPGIU	437
Db	1459	CTCAGACCACCTTCAAGCCCAAGGATCAAGTCAAGTCAACCAAGTATTTTGAATGAG	1518
QY	438	GLUPHERTRALAGINTHRIETHRIIETHRPROROGIULYSYTRYASPGIUAASPGIYMET	457
Db	1519	GAGTTCAAGGCCAGATGATCAACATCAACCAACTGTACAA-----GATGACAGCATG	1572

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0Y      458 Aapcyaskecshapangluatgaagpccrohhapherocglhphsercyltyserlaser 476
Db      1573 GAGTGTGTGACGACGAGCCGACGCCCCCACTTCCCCAGATTCTCTACTGCGCCAGC 1629

RESULT 7
US-09-023-655-1206
; Sequence 1206, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Sellmer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2610 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g190827
US-09-023-655-1206

Alignment Scores:
Pred. No.:          6,73e-236      Length:      2610
Score:              2099.50         Matches:      396
Percent Similarity: 90.19%          Conservative: 36
Best Local Similarity: 82.67%       Mismatches:   42
Query Match:        82.08%          Indels:       5
                        4              Gaps:           4

US-09-869-079B-3 (1-479) x US-09-023-655-1206 (1-2610)
0Y      1 MetSerAspValThrIleValIysGIuGIYTPVaIglNtLYeArgGIyGJutYrIleIys 20
Db      199 ATGAGCAcAGTGGCTATTGTGAAGAGGAGGTGGCTCAcAAACGAGGGAGTACATCAG 255
0Y      21 AsnTPtrArgProArgTYrPheLeuLeuLYsrThAspGIYSerPheIleGIYTYrIysGIu 40
Db      259 ACCTGGCGGCGCACGCTCTCTCTCCACAGAAATGATGGACCTTCATTGGCTACAGAG 310
0Y      41 LYsrProclnAspValAsp--LeuProTYrProLeuAsnAsnPhSerValAlaIysCys 59

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Db	319	CGGCCGAGAGTGTGAGCAACAGTGAAGGCTCCCTCAACAACTTCTCTGTGGCGAAGTGC	378
QY	60	GIuNeuMeLySThGIuArProLySPrOaAnThrPheIleIeArGYSLeuGIuInTPR	79
Db	379	CAGCTGATGAAGACGAGACGGGCCCGGCCCAACCTTCATCATCTCGCTGCCTGAGTGG	438
QY	80	ThrThrValIIeGIuArGThrPheHisValAspThrProGIuArGIuGIuInTPRThr	99
Db	439	ACCACTGTCAATCGAACCGCACTTCATGTGAGACTCTGTGAGAGCCGGAGAGATGGACA	498
QY	100	GIuAlaIleGIuAlaValAlaAspArgLeuGIuArGIuGIuGIuGIuArGMeAsnYS	119
Db	499	ACCCGCATCCAGACTGTGGCTGACGGCTTCAGAAACAGAGAGAGAGAGATGACCTTC	558
QY	120	SePProThrSerGIuIleAspAsnIIeGIyGIuGIuGIuMeAspAlaSerThrThrHis	139
Db	559	CGGTGGGGCTACCCAGTACACACTCGAGGGGCTGAGAGATGAGAGTGTCTCCGTGGCAAG	618
QY	140	HiSlYS--AAGLySThrMeCAsnAspPheAspTYrLeuLySLeuLeuGIyLySGLyThr	158
Db	619	CCCAAGACCCCGTGAACCATGAAGAGAGTTTGAATCACTGAAGCGTGTGGGCAAGGGCACT	678
QY	159	PheGIyLySValIIeLeuValArgGIuLySAlaSerGIyLySTYrTYrAlaMeCYSIle	178
Db	679	TTCCGCAGATGATCTCTGTGTAGAGAGAGAGCCACAGGCCCTACTACGCAATGAAGATC	738
QY	179	LeuLySLySGIuValIIeIleAlaLySAspGIuValAlaHisThrLeuThrGIuSerArg	198
Db	739	CTCAAGAAAGAAAGTATCATGTGTGCCAAGAGCAGAGTGGCCACACTACCGAAGAACCGC	798
QY	199	ValLeuLySAsnThrArgHisIAspPheLeuThrSerLeuLySTYrSerPheGIuInThrYS	218
Db	799	GTCTGTGACGAACCTCGAGGACCCCTTCTCTCACAGCCCTGAAGTACTCTTTCAGACCCAC	858
QY	219	AspArgLeuCYsPheValMeCGLuTYrValaLenGIyGIyLeuPhePheHisIleuSer	238
Db	859	GACCGCCTCTGTCTTGTATGAGATGCCCAACGGGGCGAGCGTGTTCCTCACCTGTGCC	918
QY	239	ArgGIuArGValPheSerGIuAspArgThrArgPheTYrGIyAlaGIuIleValSerAla	258
Db	919	CGGAGACTGTGTCTCTCGAAGAACGGGCCCGGCTTCTATGGCGCTGAGATTGTGTCAACC	978
QY	259	LeuAspTYrIleuHisSerGIyLyS--IIeValTYrArgAspLeuLySLeuGIuAsnLeu	277
Db	979	CTGAGACTACCTGCAGCTCGAGAAAGAACGTGGTGTACCGGGACCTCAAGCTGAGAACCTTC	1038
QY	278	MeCLeuAspLySAspArgLyHisIleIaLySIIeThrAspPheGIyLeuCYyLySGLuGIyIle	297
Db	1039	ATGCTGTGACAAAGACGGGACATTTAAGATCAACAATTCGGGCGTGTGAAAGAGGGGATC	1098
QY	298	ThrAspAlaIaIaTrMeLySThrPheCYsGIyThrProGIuTYrLeuAlaProGIuValI	317
Db	1099	AAGAGCGGTGCCACATGAAGACTTTTGGGGCACACTGAGTACTGTGCCCCCGAGGTG	1158
QY	318	LeuGIuAspAsnAspTYrGIyArgAlaValaAspTYrProGIyLeuGIyValIaMeCYSYr	337
Db	1159	CTGAGAGACATGACTACAGCGCCGTGACGTGATCGTGGGGGCTGGGGGTGTGATGATAC	1218
QY	338	GIuMeCYSySGLyArgLeuProPheTYrAsnGIuAspHisGIyLySLeuPheGIuLeu	357
Db	1219	GAGATGATGTGGGTGGCGCTGCCCTTCTTAACAACAGACCAATGAGAAGCTTTTGAAGCTC	1278
QY	358	IIeLeuMeCGLuAspIleLySPhPProArgThrLeuSerSerAspAlaLySeriLeuLeu	377
Db	1279	ATCTCTATGAGAGAGATCCGCTTCCCGGCACGCTTGGTCCCGAGGCCAAGTCTTGTCTT	1338
QY	378	SerGIyLeuLeuIleLySAspProAsnLySArgLeuGIyGIyGIyProAspAspAlaLyS	397
Db	1339	TCAGGGGCTGTCAAGAAAGAACCCCAACAGAGGCTTGAGCGGGGGCTCCGAGAGACGCCAAG	1398
QY	398	GIuIIeMeCArgHisSerPhePheSerGIyValaAsnTPRGIuAspValTYrAspLyLyS	417
Db	1399	GAGATCATGTAGCAATCGCTCTTGTGGCGATATCGTGTGGCAGCACGTGTACGAAGAGAG	1458

QY 418 LeuValProProPhelysProGluValThrSerGluThrAspThrArgTyrPheAspGlu 437
DB 1459 CTCAGGCCACCTTCAAGCCCGGAGTCACGTCGAGACTGACACCGATTTTGTATGAG 1518
QY 438 GluPheThrAlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMet 457
DB 1519 GAGTTTACCGCCCGCATGTATGATCACCATCACACCTGACCA-----GATGACAGCATG 1572
QY 458 AspCysMetAspAspGluArgArgProHisPheProGlnPheSerTyrSerAlaSer 476
DB 1573 GAGTGTGTGACAGGAGGCGACGCGCCACTTCCCGAGTTCTCTACTGCGCCAGC 1629

RESULT 8
US-09-590-740-1
; Sequence 1, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-590-740-1

Alignment Scores:

Score: 6,73e-236 Length: 2610
Percent Similarity: 2099.50 Matches: 396
Best Local Similarity: 90.19% Conservative: 36
Query Match: 82.67% Mismatches: 42
Query Match: 82.08% Indels: 5
DB: 4 Gaps: 4

US-09-869-079b-3 (1-479) x US-09-590-740-1 (1-2610)

QY 1 MetSerAspValThrIleValGluGluGluGluGluGluGluGluGluGluGluGluGlu 20
DB 199 ATGACGACGCTGCTATGTTGAGAGAGGTTGCTGACAAAGAGGAGGATCATCAAG 258
QY 21 AsnTTPArgProArgTyrPheLeuLeuLysTyrAspGlySerPheIleGluTyrLysGlu 40
DB 259 ACCGTGCGGCGACGCTACTCTCTCCCAAGATGATGCGACCTTCACTGCTCAAGAGAG 318
QY 41 LysProGlnAspValAsp---LeuProTyrProLeuAspAspPheSerValAlaLysCys 59
DB 319 CGGCGCCAGATGTGACCAACGTCGAGCTCCCTCAACACTTCTGTGGCGCAGTC 378
QY 60 GlnLeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTyr 79
DB 379 CAGCTGATGAGAGCGAGGCGCGCCGCGCCCAACCTTATATCCGCTGCGCTGAGTGG 438
QY 80 ThrThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTyrThr 99
DB 439 ACCACGTGTATCCAGACGACCTTCCATGTGAGACTCTGAGAGAGCGGAGGAGTGGACA 498
QY 100 GluAlaIleGlnAlaValAlaAspArgLeuGlnArgGluGluGluGluGluGluGluGlu 119
DB 499 ACCGCAATCCAGCTGTGGCTGAGCGCTCCAAAGACAGAGAGAGAGAGAGATGAGCTTC 558
QY 120 SerProThrSerGlnIleAspAsnIleGluGluGluGluGluGluGluGluGluGluGlu 139
DB 559 CGGTGGGGCTACCACTGAGCACTCAGGGCGTGAAGAGATGAGAGTGTCTCCGCGCAAG 618
QY 140 HisLys---ArgLysThrMetAspPheAspTyrLysLysLysLysLysLysLysLysLys 158

DB 619 CCCAAGCACCGGTCGATGACATGACGATTGTGATCTGTAAGCTGCTGGGCAAGGCACT 678
QY 159 PheGlyLysValIleLeuValArgLysLysAlaSerGlyLysTyrTyrAlaMetLysIle 178
DB 679 TTCGGCAAGTATCTCTGTGTGAGAGAGAGGCGCGCTTACTTACCCATGAGATC 738
QY 179 LeuLysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArg 198
DB 739 CTCAGAGAGAGATGATGCTGTCGCAAGAGCGAGGTGGCCCAACATCACTCAGAGAACCC 798
QY 199 ValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLys 218
DB 799 GTCTGCAAGATCTCAGGACCCCTTCTCAGACGCTGTAAGTACTCTTCCAGACCCAC 858
QY 219 AspArgLeuCysPheValMetGluTyrValaAsnGlyGluLeuPhePheHisLeuSer 238
DB 859 GACCGCTTCTGCTTGTCTATGAGATGACGCAACGGGGGAGCTGTTCTTCACTGTTC 918
QY 239 ArgGluArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAla 258
DB 919 CGGAAACGTGTCTTCCGAGAGACCGGGCCGCTTCTATGCGGTGAGTTGTGTACGCC 978
QY 259 LeuAspTyrLeuHisSerGlyLys---IleValTyrArgAspLeuLysLeuGluAsnLeu 277
DB 979 CTGGACTACTCTGCTCGAGAGAACGCTGTGTACCGGACCTCAAGCTGAGAACCTTC 1038
QY 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIle 297
DB 1039 ATGCTGACAAAGAGCGGCACTTAAATGATCAGACGCTGCGGCTGTGCAAGAGGAGATC 1098
QY 298 ThrAspAlaIleThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluVal 317
DB 1099 AAGACGCTGCGCACATGAGACCTTTGCGGACACCTGAGTACTGCGCCCGAGGAG 1158
QY 318 LeuGluAspAsnAspTyrGlyArgAlaValAspTyrTyrGlyLysGlyValValMetTyr 337
DB 1159 CTGAGAGAAAGATGACGCGCTGACGAGCTGCTGAGGCTGCGGTGTCTGTATC 1218
QY 338 GluMetMetCysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeu 357
DB 1219 GAGATGATGTGCGGTGCGCTGCTCTTCAACACGAGACATGAGAGCTTTTAACTTC 1278
QY 358 IleLeuMetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377
DB 1279 ATCTCATGAGAGAGATCGCTTCCGCGCAGCTTGGTCCGAGGCCAAGCTTGGCT 1338
QY 378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyLysProAspAspAlaLys 397
DB 1339 TCAGGGCTGTCTCAAGAGAGACCCCAAGAGAGCTTGGCGGGGCTCCGAGGAGCGCCAG 1398
QY 398 GluIleMetArgHisSerPheSerGlyValaAsnTyrGlnAspValTyrAspLysLys 417
DB 1399 GAGATCATGACACATCGCTTCTTCCGCTATCGTGTGACACGCTTACAGAGAGAG 1458
QY 418 LeuValProProPhelysProGluValThrSerGluThrAspThrArgTyrPheAspGlu 437
DB 1459 CTCAGGCCACCTTCAAGCCCGGAGTCACGTCGAGACTGACACCGATTTTGTATGAG 1518
QY 438 GluPheThrAlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMet 457
DB 1519 GAGTTTACCGCCCGCATGTATGATCACCATCACACCTGACCA-----GATGACAGCATG 1572
QY 458 AspCysMetAspAspGluArgArgProHisPheProGlnPheSerTyrSerAlaSer 476
DB 1573 GAGTGTGTGACAGGAGGCGACGCGCCACTTCCCGAGTTCTCTACTGCGCCAGC 1629

RESULT 9
US-09-256-465-1
; Sequence 1, Application US/09256465
; Patent No. 6043090
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowbert

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; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; FILE REFERENCE: RTS-0035
; CURRENT APPLICATION NUMBER: US/09/256,465
; CURRENT FILING DATE: 1999-02-23
; SEQ ID NO 1
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (88)..(1533)
; US-09-256-465-1

Alignment Scores:
Pred. No.: 5,156-225 Length: 1599
Score: 2004.00 Matches: 374
Percent Similarity: 88.84% Conservative: 56
Best Local Similarity: 77.27% Mismatches: 46
Query Match: 78.34% Indels: 8
DB: 3 Gaps: 5

US-09-869-079b-3 (1-479) x US-09-256-465-1 (1-1599)

Qy 1 MetSerArgValThrIleValIysGluGlyTrpValGlnIysArgGlyIuTyrlle 20
Db 88 ATGATAGAGTGTCTGATCATCAAGAGAGGCTGGCTCCACAGAGCTGGTAATCATAG 147
Qy 21 AsnTrpArgProArgTyrPheLeuLeuLysThrAspLysSerPheIleGlyTyrLysGlu 40
Db 148 ACCTGAGAGCCACGGTACTTCTGCTGAGAGCGAGCGCTCTTCATTGGGTACAGAG 207
Qy 41 LysProGln-----AspValAspLeuProTyrProLeuAsnAspSerValAlaLys 58
Db 208 AGGCCCCAGGCCCCCTGATCAGACTTACC---CCCTTAACAACCTTCTCGTAGCAGAA 264
Qy 59 CysGlnLeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGln 78
Db 265 TGGCAGCTGATGAGAGCCGAGAGCCGAGACCCAAACCTTTGTCATACCTGCTGACG 324
Qy 79 TrpThrValIleGluArgThrPheIleValAspThrProGlnGluArgGluGluTrp 98
Db 325 TGGACCACTGATCGAGAGAGACTTCCAGTGGATTCTCCAGACGAGAGGAGAGTGG 384
Qy 99 ThrGluAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGlu-----GluGluArg 116
Db 385 ATCGGGCCCATCCAGATGTCGCCCAACAGCCCTCAAGAGCGGCCCCAGCGAGAGCC 444
Qy 117 MetAsnCysSerProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSer 136
Db 445 ATGGACTACAAAGTGTGGCTCCCCAGTACTCTCCACGAGCTGAGGAGATGAGAGTGG 504
Qy 137 ThrThrIshIleLysArgLys---ThiMetAsnAspPheAspTyrLeuLysLeuGly 155
Db 505 GTGAGCAAGGACAGGGGTAAAGAGCAATGATGACTTCATCTCAATCTCAATCTCTTGG 564
Qy 156 LysGlyThrPheGlyLysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAla 175
Db 565 AAGGGAACCTTTGGCAAGTCATCTGCTGGGAGAGGCACTGGCCCTACTAGGCC 624
Qy 176 MetLysIleLeuLysLysGluValIleIleAlaLysAspGluValAlaIshIleThrLeuThr 195
Db 625 ATGAAATCTCTGGAAAGAGATCATATGCTCCAGAGATGAGTGCCTCACACAGTACC 684
Qy 196 GluSerArgValIleuLysAsnThrArgIshProPheLeuThrSerLeuLysTyrSerPhe 215
Db 685 GAGAGCGCGGTCTCTCCAGAACACACAGGACCCGTTCTCACTGGCGAGATGCTTCC 744
Qy 216 GlnThrLysAspArgLeuCysPheValMetGluTyrValAsnGlyLysGluLeuPhePhe 235
Db 745 CAGACCCACACAGCGCTGTGCTTGTGATGAGATGCCAAACGGGGGTGAGCTGCTTCT 804
Qy 236 HisLeuSerArgGluArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIle 255

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Db 805 CACCTGCCCCGAGAGGCTGCTTACAGAGAGACGGCCGGTTTATGTCAGAGATT 864
Qy 256 ValSerAlaLeuAspTyrLeuLysSerGlyLysIleValTyrArgAspLeuLysGlu 275
Db 865 GTCTCGGCTCTTGAATGACTTGCAGCTCGCGGAGCGTGTATACCGGACATCAAGCTGAGAA 924
Qy 276 AsnLeuMetLeuAspLysAspGlyIshIleLysIleThrAspPheGlyLeuCysLysGlu 295
Db 925 AACCTCATGTGAGCAAGATGGCCATCAATCAATCATGACTTGGCTTCCCAAGAG 984
Qy 296 GlyIleThrAspAlaIleThrMetLysThrPheCysGlyThrProGluTyrLeuAlaPro 315
Db 985 GGCATCAGTACGAGGAGCCAGCAATGAAACCTTCTGTGGAGACCCCGAGTACTGGCGCT 1044
Qy 316 GluValIleuGluAspAsnAspTyrGlyArgAlaValAspTrpTyrGlyLeuGlyVal 335
Db 1045 GAGGTCTGGAGAGCAATGACTTATGCGCGGCGCTGAGACTGTGGGGGCTGGGTGTGTC 1104
Qy 336 MetTyrGluMetMetCysGlyArgLeuProPheTyrAsnGlnAspIshIleLysGluLeuPhe 355
Db 1105 ATGTACGAGATGATGTGCGCGCCGCTGCTTCTACACAGGACACAGAGCGCTTCTC 1164
Qy 356 GluLeuIleLeuMetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSer 375
Db 1165 GAGCTATCTCTATGAGAGAGATCCGCTTCCGCGAGCTGACGCCCGAGGCAAGTCC 1224
Qy 376 LeuLeuSerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyProAspAsp 395
Db 1225 CTGCTTGCGGTGCTGTAAAGAGACCCCAAGACAGAGGCTTGTGGGGGCCACAGAT 1284
Qy 396 AlaLysGluIleMetLysIshSerPhePheSerGlyValAsnTrpGlnAspValTyrAsp 415
Db 1285 GCCAAGAGAGTCAATGAGACAGAGTCTTCTCAGCATCAACTGAGAGACGCTGTCCAG 1344
Qy 416 LysLysLeuValProProPheLysProGlnValIshSerGlyThrAspThrArgTyrPhe 435
Db 1345 AAGAGCTCTGTCACCTTCAACCTCAAGTACGTCGAGGTGACACAGAGTACTTC 1404
Qy 436 AspGluGluPheThrAlaGlnThrIleThrIleThrProGluLysTyrAspGluAsp 455
Db 1405 GATGATGAATTTACCGCCAGCTCATCAATCAATCAACACCCCTGACCGCTATGACAGCTG 1464
Qy 456 GlyMetAspCysMetLysAsnGluArgArgProIshPheProGlnPheSerTyrSerAla 475
Db 1465 GGGCTTA-----CTGAGGCTGACGACGAGACCCAGCTTCCCACTGCTGAGGCC 1518
Qy 476 SerGlyArgGlu 479
Db 1519 AGCATCCGCGAG 1530

RESULT 10
US-09-167-322-3
; Sequence 3, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Seidel, Gonda, Lavoigna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/167,322
FILING DATE: 07-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/00582
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 7933-33 PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1599 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-167-322-3
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Alignment Scores:
Pred. No.: 5,15e-225 Length: 1599
Score: 2004.00 Matches: 374
Percent Similarity: 88.84% Conservative: 56
Best Local Similarity: 77.27% Mismatches: 46
Query Match: 78.34% Indels: 8
DB: 3 Gaps: 5
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US-09-869-079b-3 (1-479) x US-09-167-322-3 (1-1599)

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QY 1 MetSerAspValThrIleValysGluGlyTrpValGlnIlyAspGlyGluIlyrIleIys 20
DB 88 ATGAATGAGGTGCTGTCTCATCAAGAGCGTGCACAGCGTGCTGTAATACATCAAG 147
QY 21 AsnTrpArgProArgTrpPheLeuLeuIysThsAspGlySerPheIleGlyTrpIlyGln 40
DB 148 ACCTGAGAGCCACGATCTTCCCTGCTGAAGAGAGCGCTCTTCACTTGGGTCAGAG 207
QY 41 LysProGln-----AspValAspLeuProTrpTrpLeuAsnAsnAsnSerValAlaLys 58
DB 208 AGCGCCGAGCGCCCTTATCATCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 264
QY 59 CysGlnLeuMetIleThrGluArgProIlyProAsnThrPheIleIleArgCysLeuGln 78
DB 265 TGCACGCTGATGAAGACCGAGAGCGCGACCCACACACCTTGTCTACGCTGCTGCAG 324
QY 79 TrpThrThrValIleGluArgThrPheHlsValAspThrProGluGluArgGluIlyTrp 98
DB 325 TGGACCAAGCTCATCGAGAGGACCTTCCACGTGATTTCTCCAGACGAGAGGAGAGTGG 384
QY 99 ThrGluAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnIly-----GluGluArg 116
DB 385 ATGCGGGCGATCGAGTGGTGGCCCAACAGCTCAACAGCGGCGCCACAGCGAGAGCCCC 444
QY 117 MetAsnCysSerProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSer 136
DB 445 ATGGACTTACAGTGGCTCCCGCCAGTGACTCTCCACGACGTAGAGAGTGAAGTGGGG 504
QY 137 ThrThrHlsHlsIleLysArgLys---ThrMetAsnAspPheAspTrpLeuIlyLeuGly 155
DB 505 GTCAGACGAGCAGCGGCTTAAGAGACCAATGAATGACTTGCACATCTCAAACTCTTGGC 564
QY 156 LysGlyThrPheGlyLysValIleLeuValArgGluLysAlaSerGlyLysTrpYrAla 175
DB 565 AAGGGAACCTTTGGCAAGTCATCTGTGGCGGAGAAAGGCGCACTGGCGCTACTAGCCG 624
QY 176 MetLysIleLeuLysIleGluValIleIleAlaLysAspGluValAlaHlsThrLeuThr 195
DB 625 ATGAAGATCCTGGAAAGAGATCATCTATTGCCAAGAGTGAATGCTCTCACACAGTCCAC 684
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QY 196 GluSerArgValLeuLysAsnThrArgHlsProPheLeuThrSerLeuLysTrpSerPhe 215
DB 685 GAGAGCCGGGTCTCTCAGAGACACAGAGCCCGGTCTCTCACTGCGCTGAAGATGCTTCC 744
QY 216 GlnThrLysAspArgLeuCysPheValMetGluTrpValAsnGlyGlyGluLeuPhePhe 235
DB 745 CAGACCCACGACCGGCTGTGTGTGATGAGTATGCCAACGGGGGTGAGCTGTCTTCC 804
QY 236 HlsLeuSerArgGluLysArgValPheSerGluAspArgThrArgPheTrpGlyValIle 255
DB 805 CACCTGCTCCGGAGAGGTCTTCAACAGAGAGCGGCGCGGCTTTATGTCACAGATT 864
QY 256 ValSerAlaLeuAspTrpLeuHlsSerGlyLysIleValTrpArgAspLeuLysLeuGln 275
DB 865 GTCTGGGCTCTTGAGTACTTGACCTCGCGGAGCGGTATACCGGAGATCAAGCTGGAA 924
QY 276 AsnLeuMetLeuAspLysAspGlyHlsIleLysIleThrAspPheGlyLeuCysLysGln 295
DB 925 AACCTATGCTGGAACAAAGATGCCACATCAAGATCACTGACTTGGCTTGCACAAAG 984
QY 296 GlyIleThrAspAlaAlaThrMetLysThrPheCysGlyTrpProGluTrpLeuAlaPro 315
DB 985 GGATCATGAGTACGGGCGCACATGAATACCTTGTGGACCCCGAGTACTGGCGCTT 1044
QY 316 GluValLeuGluAspAsnAspTrpGlyArgAlaValAspTrpTrpGlyLeuGlyValVal 335
DB 1045 GAGGTGCTGGAAGACATGATGATGCGCGCGCGGTGAGTGGTGGGGCTGGGTGGTGC 1104
QY 336 MetTrpGluMetMetCysGlyLysArgLeuProPheTrpAsnGlnAspHlsGlyLysLeuPhe 355
DB 1105 ATGTACGAATATGTGCGCGCGCTGCTGCTTCAACACAGACACACAGCGCGCTTTC 1164
QY 356 GluLeuIleLeuMetGluAspLysPheProArgTrpLeuSerSerAspAlaLysSer 375
DB 1165 GAGCTCATCTCATGGAAGATCGGCTTCCGCGACCTTACAGCCCGGAGGCCAAGATTC 1224
QY 376 LeuLeuSerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyGlyProAspAsp 395
DB 1225 CTGCTTGCTGGGCTGCTTGAAGAGGCCACCAAGAGAGCTTGTGGGGGCGCAGCAT 1284
QY 396 AlaLysGluIleMetArgHlsSerPhePheSerGlyValAsnTrpGlnAspValTrpAsp 415
DB 1285 GCCAAGAGATGATGAGCAGCAGGTTCTTCCACAGATCACTGCGAGGACGCTGTCAG 1344
QY 416 LysLysLeuValProProPheLysProGlnValThrSerGlnThrAspThrArgTrpPhe 435
DB 1345 AAGAGCTCTGCAACCTTCAACCTCAGGTACAGTCCGAGGTGACACAGATCTTCC 1404
QY 436 AspGluGluPheThrAlaGlnThrIleThrIleThrProProGluLysTrpAspGluAsp 455
DB 1405 GATGATGAATTTACGGCCAGTCCATCAATCAACACCCCTGACCGGTATGACAGCTTC 1464
QY 456 GlyMetAspCysMetAspAsnGluArgArgProHlsPheProGlnPheSerTrpSerAla 475
DB 1465 GGCTTA-----CTGAGAGTGAACGACGAGCGACCACTTCCCAAGTTCCTACTCGGCC 1518
QY 476 SerGlyArgGlu 479
DB 1519 AGCATCGCGGAG 1530

RESULT 11
US-09-023-655-1004
Sequence 1004, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cooke, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
```



```
RESULT 12
US-09-590-740-3
; Sequence 3, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-590-740-3

Alignment Scores:
Pred. No.: 4,72e-201 Length: 1254
Score: 1798.50 Matches: 342
Percent Similarity: 89.45% Conservative: 31
Best Local Similarity: 82.01% Mismatches: 39
Query Match: 70.31% Indels: 5
DB: 4 Gaps: 4

US-09-869-079B-3 (1-479) x US-09-590-740-3 (1-1254)

QY 62 MetLysThrGluArgProLysProAsnThrPheIleArgCysLeuGlnTrpThr 81
DB 1 ATGAAGACGGAGGGCCCGCCGACCAACCTTCATCATCGCGCTGCGAGGACCACT 60
QY 82 ValIleGluArgThrPheHisValAspThrProGluGluArgGluGlnTrpThrGluAla 101
DB 61 GTCATCGAAGCAGCACTTCATGAGAGCTCTCGAGAGCGGAGAGAGAGCAACCGCC 120
QY 102 IleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCysSerPro 121
DB 121 ATCCAGACTGTGGCCGACCGCTCAAGAAAGCAGAGAGAGAGAGATGACCTTCGGGTG 180
QY 122 ThrSerGlnIleAspAsnIleGluGluGluMetAspAlaSerThrHisIleLys 141
DB 181 GGTCTACCCAGGACCACTCAGGGGCGCAAGAGATGAGGTGCTCGGCCAAGCCCAAG 240
QY 142 ---ArgLysThrMetAsnAspPheAspTrpLeuLysLeuLeuGluLysGlyThrPheGly 160
DB 241 CACCGCGGTGACCATGAGCAAGTTTGATGCTGACCTGCGGCAAGGCGACTTTCGCG 300
QY 161 LysValIleLeuValArgLysValAspArgLysTrpTrpAlaMetLysIleLeuLys 180
DB 301 AAGGTGATCTGCTGTAAGAGAGAGGCGCACAGCG--TACTAGCGCCATGAGATCTTCAG 357
QY 181 LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArgValLeu 200
DB 358 AAGGAAGTCATGCTGCGCAAGAGCGAGTGGCCCAACACTCAGAGAACCGGCTCAG 417
QY 201 LysAsnThrArgHisProPheLeuThrSerLeuLysTrpSerPheGlnThrLysAspArg 220
DB 418 CAGAACTCCAGGACCCCTCTCTCACTCCCTGAACTACTCTTTCAGAGCCACGACCGCC 477
QY 221 LeuCysPheValMetGluTrpValaAsnGlyGluLeuPhePheHisLeuSerArgGlu 240
DB 478 CTCTGCTTTGTCTATGAGAGTACGCCAAGGGGGGAGACTGTTCTTCACCTGTCGGGAG 537
QY 241 ArgValPheSerGluAspArgThrArgPheTrpGlyAlaGluIleValSerAlaLeuAsp 260
DB 538 CGGTGTTGCGCGAGAGACCGGGCGGCTTCTATGCGCTGAGATTGTGCAAGCCCTGAG 597
QY 261 TrpLeuHisSerGlyLys---IleValTrpArgAspLeuLysLeuGluLeuLeuMetLeu 279
DB 598 TACCTGCACTCGAAGAAAGACGTGTATCCGGGACCTCAAGCTGAGAACTCATGCTG 657
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QY 280 AspLysAspGlyHisIleLeuThrAspPheGlyLeuCysLeuGluGlyIleThrAsp 299
DB 658 GACAAAGACGGGCACTTAAATCAACACTTCGGGCTGTGTGCAAGAGGAGTCAAGAC 717
QY 300 AlaAlaThrMetLysThrPheCysGlyThrProGluTrpLeuAlaProGluValLeuGlu 319
DB 718 GGTGCACCATTAAGACCTTTGGCGGACACTGTAGTACTGGCCCGGAGGTGTGGAG 777
QY 320 AspAsnAspTrpGlyArgAlaValAspTrpTrpGlyLeuGluValValMetTrpGluMet 339
DB 778 GACAAATGACTACGGCGGTGAGTGTGGGGGCTGGGGGTGTCTATGTACAGAGATG 837
QY 340 MetCysGlyArgLeuProPheTrpAsnGlnAspHisGluLysLeuPheGluLeuLeu 359
DB 838 ATGTGCGGTGCGCTCCCTCTACCAACAGACCATGAGAGCTTTTGAGCTACTCTC 897
QY 360 MetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGly 379
DB 898 ATGAGAGAGATCCGCTCCCGGACGCTTGATCCCGAGGCCAAGTCTTGCTTCAAGG 957
QY 380 LeuLeuIleLysAspProAsnLysArgLeuGlyGlyTrpProAspAspAlaLysGluIle 399
DB 958 CTGCTCAAGAAAGACCCCAAGCAGAGCTTGCGGGGCTCGAGCAGCGCCAAAGAGATC 1017
QY 400 MetArgHisSerPhePheSerGlyValaAsnTrpGlnAspValTrpAspLysLeuVal 419
DB 1018 ATGCAAGATCGCTTTTACCGGTATCGTGTGCGACGACGTGTACAGAAAGAGCTCAGC 1077
QY 420 ProPheLysProGluValaThrSerGluThrAspThrArgTrpPheAspGluLysPhe 439
DB 1078 CCACCTTCAAGCCCAAGGTCACTGCGAGACTGACACCAAGATATTGTATGAGAGATTC 1137
QY 440 ThrAlaGlnThrIleThrIleThrProGluLysTrpAspGluAspGlyMetAspCys 459
DB 1138 ACGGCCAGATGATCAATCAACACTGACCAA-----GATGACAGCATGAGATGT 1191
QY 460 MetAspAsnGluArgArgProHisPheProGlnPheSerTrpSerAlaSer 476
DB 1192 GTGCAAGAGAGCGAGGCGCCCACTTCCCGCACTTCTCTACTCCGCCACAGC 1242

RESULT 13
US-10-067-977-1
; Sequence 1, Application US/10067977
; Patent No. 6830911
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua and KE, Zhaoxi
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; FILE REFERENCE: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C1001313
; CURRENT APPLICATION NUMBER: US/10/067,977
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1338
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-067-977-1

Alignment Scores:
Pred. No.: 2.1e-97 Length: 1338
Score: 916.00 Matches: 193
Percent Similarity: 60.75% Conservative: 67
Best Local Similarity: 45.09% Mismatches: 140
Query Match: 35.81% Indels: 28
DB: 4 Gaps: 7

US-09-869-079B-3 (1-479) x US-10-067-977-1 (1-1338)

QY 53 AsnPheSerValAlaLysCysGlnLeuMetLysThrGluArgProLysProAsnThrPhe 72
DB 53 AsnPheSerValAlaLysCysGlnLeuMetLysThrGluArgProLysProAsnThrPhe 72
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Db 97 TCCTTCCTGCTGACGGGACTGGCTTTCATGAGACAGAGAGATGGGCTGACAGCACTTT 156
 QY 73 ILeIeArgCySleuGlnTrpThrValIleGluArgThrPheHisValAspThrPro 92
 Db 157 ATTCCAGAAAG-----ATTGCCAATTAATCTCATGATGATCAAAACACCTT 198
 QY 93 GluGluArgGluGluTrpThrGluAlaIleGlnAlaValAlaAspArgLeuGlnArgGln 112
 Db 199 GAA-----GTTCAAGTCATCTTGAAGATCTCCCAACCTCAG 234
 QY 113 GluGluGluArgMetAspCysSerProThr-----SerGlnIleAspAsn 127
 Db 235 GAGCCTGAGCTTATGAATGCCACCTCTCTCCACCAAGCTCTTTCAGCAATAC 294
 QY 128 ILeGlyGluGluGluMetAspAlaSerThrHisHisValAspArgLysThrMetAspAsp 147
 Db 295 CTGGC-----CCGTCGTCATCTCATCTCTAA-----CCATCTGAC 333
 QY 148 PheAspTrpLeuLeuLeuLeuGlyValGlyThrPheGlyValIleLeuValArgGlu 167
 Db 334 TTTCACCTCTTGAAGAGTATGCGAAGGAGGAGTTGGAAAGTTCTTTCAGCAAGCAC 393
 QY 168 LysAlaSerGlyLysTrpTrpAlaMetValIleLeuLysGluValIleIleAlaLys 187
 Db 394 AAGGCAGAAAGAGTCTTATGCAATGCAATTTTACAGAAAGAAAGCAATCTCGAAAG 453
 QY 188 AspGluValAlaHisThrLeuThrGluSerArgVal---LeuLysAsnThrArgHisPro 206
 Db 454 AAGAGAGAGAAAGCATATTATGTCGAGACGGAATGTTCTGTTGAAGATGAGAGACCTT 513
 QY 207 PheLeuThrSerLeuLysTrpSerPheGlnThrLysAspArgLeuCysPheValMetGlu 226
 Db 514 TTCTCTGGTGGCCCTTCACTTCTCTTCCAACTGCTGACAAATTTGACTTGTTCCTAGAC 573
 QY 227 TyrValAsnGlyGlyGluLeuPhePheHisLeuSerArgGluArgValPheSerGluAsp 246
 Db 574 TACATTAATGTGTGAGAGTGTCTTACCACTCCAGAGGAAACCTGCTTCTCGGAACCA 633
 QY 247 ArgThrArgPheTrpGlyAlaGluIleValSerAlaLeuAspTrpLeuHisSerGlyLys 266
 Db 634 CGGGCTGCTTCTATGCTGCTGAAATGACCAAGTCCCTGGGCTACGCAATTCACCTGAC 693
 QY 267 IleValTyrTrpArgPheLysLeuGluAsnLeuMetLeuAspLysAspGlyHisIleLys 286
 Db 694 ATGGTTTATGAGACTTAAACCAAGAAATATTTGCTAATTCACAGGAGCACTATGTC 753
 QY 287 IleThrAspPheGlyLeuCysLysGluGlyIleThrAspAlaAlaThrMetLysThrPhe 306
 Db 754 CTTACTGACTTCCGACTCTGCAAGAGAAACATTGAACACACAGACATCCACCTTC 813
 QY 307 CysGlyThrProGluTrpLeuAlaProGluValLeuGluAspAsnAspTrpGlyArgAla 326
 Db 814 TGTGGCAGCCGCGAGTATCTCGACCTGAGGTGCTCATAGACGCTTATGACAGACT 873
 QY 327 ValAspTrpTrpGlyLeuGlyValValMetTrpGluMetMetCysGlyArgLeuProPhe 346
 Db 874 GTGAGCTGTGTGGCTCGGAGCTGTCTTATGAGATGCTGATAGGCTCGCGCCCTTTT 933
 QY 347 TyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMetGluAspIleLysPhePro 366
 Db 934 TATAGCCGAAACACAGCTGAATATGACACACATTTCGAACAAGCTCTCCAGCTGAA 993
 QY 367 ArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeuLeuIleLysAspProAsn 386
 Db 994 CCAAAATATTACAATTCGCGAAGACACCTCTCGAGGGCTCTCGCAGAAAGACAGAGCA 1053
 QY 387 LysArgLeuGlyGlyGlyProAspAspAlaLysGluIleMetArgHisSerPhePheSer 406
 Db 1054 AAGCGGCTC---GGGCGCAAGAGATCTTATGAGATTAAGAGCTCATGCTCTCTCTTC 1110
 QY 407 GlyValAsnTrpGlnAspValTyrAspLysLeuValProPheLysProGlnVal 426
 Db 1111 TTAAATTAACTGGAGTATCTCATTAATTAAGAAGTTACTCCCTTTTAAACCAAAATGTG 1170

QY 427 ThrSerGluThrAspThrArgTrpPheAspGluGluPheThrAlaGlnThrIleThrIle 446
 Db 1171 AGTGGGCCCAACACACTTACGAGCACTTGAACCCGAGATTACCAAGAGCTGTGCCAAC 1230
 QY 447 ThrProGluLysTrpAspGluAspGlyMetAspCysMetAspAsnGluArgPro 466
 Db 1231 TCCATTGGCAAGTCCCTGACAGCCCTCTGTCACAGCAAGCTCAAGAAAGCTGCCGAG 1290
 QY 467 HisPheProGlnPheSerTrpSer 474
 Db 1291 GCTTCTTACGCTTTCCTATGCG 1314
 RESULT 14
 US-09-031-295-1
 ; Sequence 1, Application US/09031295
 ; Patent No. 6326181
 ; GENERAL INFORMATION:
 ; APPLICANT: LANG, Florian
 ; APPLICANT: WALDBERGER, Tubingen
 ; TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: FOLEY & LARDNER
 ; STREET: 3000 K Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Releasee #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/031,295
 ; FILING DATE: 26-FEB-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE 197-08-173.8
 ; FILING DATE: 28-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sandercock, Colin G.
 ; REGISTRATION NUMBER: 31,298
 ; REFERENCE/DOCKET NUMBER: 058315/0123
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 672-5300
 ; TELEFAX: (202) 672-5399
 ; INFORMATION FOR SEQ. ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2370 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 43..1335
 ; US-09-031-295-1
 Alignment Scores:
 Pred. No.: 3,37e-96 Length: 2370
 Score: 909.00 Matches: 191
 Percent Similarity: 61.10% Conservative: 65
 Best Local Similarity: 45.58% Mismatches: 135
 Query Match: 35.54% Indels: 28
 DB: 3 Gaps: 7
 US-09-869-079b-3 (1-479) x US-09-031-295-1 (1-2370)
 QY 62 MetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTrpThr 81
 Db 124 ATGAAACAGAGAGAGATGGGTCTGAACGACTTATTACAGAG----- 165

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QY      82 ValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTrpThrGluAla 101
      166 ATGGCCAAATTAACCTCTATGATGATGCAAAACACCTGAA----- 201
QY      102 IleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCysSerPro 121
      202 GTTCAGTCCATCTTGAAGATCTCCCAACCTCAGAGCCTGAGCTTATGATGCAACCT 261
QY      122 Thr-----SerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSer 136
      262 TCTCTCCCAACCAAGCTCTCTCAGCAATCAACCTTGGC-----CCGTGCTCC 309
QY      137 ThrThrHisIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 156
      310 AATCCCATGCTGAA-----CCATGCACTTCACTCTTGAAGATGCAAGGAAAG 360
QY      157 GlyThrPheGlyIleValIleLeuValArgGluIleAspGlyIleIleIleIleIleIle 176
      361 GGCAGTTTGGAAAGGTTCTTCTAGACAGACACAGGAGAGAGAGAGAGAGAGAGAGAG 420
QY      177 ILeIleLeuIleIleGluValIleIleIleAlaIleAspGluValAlaHisThrLeuThrGlu 196
      421 AAAGTTTACAGAGAAAGCAATCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY      197 SerArgVal---LeuIleAsnThrArgHisProPheLeuThrSerLeuIleIleIleIle 215
      481 CGGAATGTTCTGTGGAAGATGGAAGCAACCTTCTGTGGGCTTCACTTCTCTTC 540
QY      216 GlnThrIleAspArgLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIle 235
      541 CACAGCTGAGCAAAATTTGCTTCTTCTGCTGAGTCACTATGATGAGAGAGTGTCTAC 600
QY      236 HisLeuSerArgGluArgValPheSerGluAspArgThrArgPheIleGlyIleGluIle 255
      601 CATCTCAGAGGAGAGAGCTGCTCTGGAACCAAGGCTGTTCTATGCTGTGAAATA 660
QY      256 ValSerAlaLeuAspIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 275
      661 GCCAGTGCCTTGGGCTACCTGCACTTCACTGCAATGCTTTATGAGACTTAAACCAAGAG 720
QY      276 AsnLeuMetLeuAspIleAspGlyIleIleIleIleIleIleIleIleIleIleIleIle 295
      721 AATATTTTGTATGATTCACAGGAGACATGCTCTGATTCGAGCTTCCGAGCTTCCAGAGAG 780
QY      296 GlyIleThrAspAlaIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 315
      781 AACATTGAAACAACAAGCACACATCCCTTGTGGACGCGGAGATGATCTGCACCT 840
QY      316 GluValIleGluIleAspAsnAspIleIleIleIleIleIleIleIleIleIleIleIle 335
      841 GAGTGTCTTCAATAGACGCTTATGACAGAGCTGTGAGCTGTGAGCTGTGGAGAGCTGTC 900
QY      336 MetIleGluMetMetCysGlyIleIleIleIleIleIleIleIleIleIleIleIleIle 355
      901 TTGTATGAGATGCTGTATGAGCTGCGGCTTTTATAGCGAAACACAGCTGAAATGATAC 960
QY      356 GluLeuIleLeuMetGluAspIleIleIleIleIleIleIleIleIleIleIleIleIle 375
      961 GACACATCTTCTGAAAGAGCTCTCAGCTGAAACCAATATTTCAGGAGAGAGAGAGAG 1020
QY      376 LeuLeuSerGlyLeuLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIle 395
      1021 CTCCTGAGAGGCTCTCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1077
QY      396 AlaIleGluIleMetArgHisSerPhePheSerGlyIleValAsnTrpGlnAspValIle 415
      1078 TTTCATGAGATTAAGATGATGCTCTCTCTCTTATTAATGATGAGATGATCATTAAT 1137
QY      416 ILeIleIleValIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 435
      1138 AAGAGATTAATCTCCCTTTTAAACCAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1197

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QY      436 AepGluGluPheThrAlaGlnThrIleThrIleThrProGluIleIleIleIleIle 455
      1198 GACCCGAGATTTACGGAAGAGGCTGTCCCACTCATTTGGCAAGTCCCTGACAGGCTC 1257
QY      456 GlyMetAspCysMetAspAsnGluArgArgProHisPheProGlnPheSerIleSer 474
      1258 CTCGTCACAGCCAGGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1314
DB      1258 CTCGTCACAGCCAGGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1314

RESULT 15
US-08-712-709-6
Sequence 6, Application US/08712709
Patent No. 5863780
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,709
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2311 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-08-712-709-6

Alignment Scores:
Pred. No.: 9.55e-96 Length: 2311
Score: 905.00 Matches: 191
Percent Similarity: 60.86% Conservative: 64
Best Local Similarity: 45.58% Mismatches: 136
Query Match: 35.38% Gaps: 28
DB: 2 Gaps: 7

US-09-869-079B-3 (1-479) x US-08-712-709-6 (1-2311)
QY      62 MetIleThrGluArgProIleAsnThrPheIleIleArgCysLeuGlnTrpThrThr 81
      91 ATGAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 132
QY      82 ValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTrpThrGluAla 101
      133 ATGGCCAAATTAACCTCTATGATGATGCAAAACACCTGAA----- 168
QY      102 IleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCysSerPro 121
      169 GTTCAGTCCATCTTGAAGATCTCCCAACCTCAGAGCCTGAGCTTATGATGCAACCT 228

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Search completed: April 13, 2005, 11:41:12
Job time : 263, secs

OY	122	Thr-----	SerGlnIleAspAsnIleGlyValGluGluMetAspAlaSer	136
Db	229	TCCTCCACCAAGTCCTCTTCAGCAAAATCAACTCTTGGC-----	CCGTGCTCC	276
OY	137	ThrThrHisHleArgAspGlySerHrmElaAsnAspPheAspTyrIleuLysLeuGluGlyLys	156	
Db	277	AATCGCATGCTGAAA-----	CCATGTGACTTTCACTTCTTGAAATGATGTCGAAAG	327
OY	157	GlyThrPheGlyLysValIleLeuValArgGlyLysAlaSerGlyLysTyrAlaMet	176	
Db	338	GGCAGATTGTGAAAGATTCTCTTCAGCAACACACAGGCAAGAGATGTTCTATGCAAGTC	387	
OY	177	LysIleLeuLysValIleIleIleAlaLysAspGluValAlaHisThrLeuThrGlu	196	
Db	368	AAAGTTTACAGAGAAACCAATCTCGAAAAAGAAAGAGAGATATTATGTCGAG	447	
OY	197	SerArgVal--	LeuLysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPhe	215
Db	448	CGGAATGTTCTGTGGAAGATGTGAAGCACCCCTTCTCGTGGGCTTCACCTTCCTTTC	507	
OY	216	GlnThrLysAspArgLeuGlySerPheValMetGluTyrValAsnGlyGlyLeuPhePhe	235	
Db	508	CAGACTGCTGACAAATGTACTTTGTCTTCAGACTACATTAATGATGGAAGTGTGTTCTAC	567	
OY	236	HisLeuSerArgGluArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIle	255	
Db	568	CATCTCCAGAGGGAACGCTGCTTCCTCGAACCACGGGCTCTTCTCATCTGCTGAAAAA	627	
OY	256	ValSerAlaLeuAspTyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGlu	275	
Db	628	GCCAGTGGCTTGGGCTACCTGCATTCACATCGAACATCGTTTATAGAGACTTAAACACAGAG	687	
OY	276	AsnLeuMetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuGlyValGlu	295	
Db	688	AATATTTTGTCTGATTCACAGGAGACATGTGCTTACTGACTTCGAGCTTCGAAAGAG	747	
OY	296	GlyIleThrAspAlaAlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaPro	315	
Db	748	AACATTGAAACACACAGCACACATTCACCTCTGTGGCAGCCCGAGATATCTCGACCT	807	
OY	316	GluValLeuGluAspAsnAspTyrGlyArgAlaValAspTyrTyrGlyLeuGlyValVal	335	
Db	808	GAGGTGCTTCATMACAGCCTTATACAGAGACTGTGAGATGTGTGTGCTCGGAGACTGTC	867	
OY	336	MetTyrGluMetMetCysGlyArgLeuProPheTyrAsnGluAspHisGluLysLeuPhe	355	
Db	868	TTGTATGAGATCTCTGATGCGCTGCGGCTTTTATAGCGGAAACACAGCTGAATGTCAC	927	
OY	356	GluLeuIleLeuMetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSer	375	
Db	928	GACAAACATTCTGAAACAGCCTCTCCAGCTGAAACCAAAATATTAACAATCCGACAGACAC	987	
OY	376	LeuLeuSerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyLysProAspAsp	395	
Db	988	CTCTCGAAGGGCTCTCTCGAGAGAGACAGACAAAGCGGCTC--GGGGCCAAAGATGAC	1044	
OY	396	AlaLysGluIleMetArgHisSerPhePheSerGlyValAsnTyrGluAspValTyrAsp	415	
Db	1045	TTCATGAGAGATTAAAGATCATGCTCTTCTCTCTTAATTAATCTGGAGATGATCTCAATTAT	1104	
OY	416	LysLysLeuValProProPheLysProGluValThrSerGluThrAspThrArgTyrPhe	435	
Db	1105	AAGAAGATTACTCCCTCTTTTAACCAATGAGATGGGGCCCAAGACCTACGGAACATT	1166	
OY	436	AspGluGluPheThrAlaGlnThrIleThrIleThrIleThrProProGluLysTyrAspGluAsp	455	
Db	1165	GACCCCGAGTTTACCGAAGAGCCTGTCCCAACTCATTTGGCAAGTCCCTTACAGCGTC	1222	
OY	456	GlyMetAspCysMetAspAsnGluArgArgProHisPheProGluPheSerTyrSer	474	
Db	1225	CTCGTCACAGCAGCGGTCAAGAGACCTGCGAGGCTTCTCTAGGCTTCTTCATGCG	1281	

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: April 13, 2005, 08:56:25 ; Search time 688 seconds

(without alignments)
4223.771 Million cell updates/sec

Title: US-09-869-079B-3

Perfect score: 2558

Sequence: 1 MSDVTIVKSGWVQKRGSEYIK.....MDNERRHPRQFSYASAGRE 479

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 5622541 seqs, 303355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-Q=/cgnt2_1/USPTO.spool.p/US09869079/runat_11042005_190025_13497/app_query.fasta_1.647
-Db=Published.Applications.NA -QFMT=fastcap -SUFFIX=g2n.rmpb -MINMATCH=0.1
-LOPCL=0 -LOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blosum62
-TRANS-human40.csl -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09869079 @CGN_1_1723 @runat_11042005_190025_13497
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=10 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications_NA: *
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3: /cgnt2_6/prodata/2/pubpna/US06_NEW_PUB.seq: *
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7: /cgnt2_6/prodata/2/pubpna/US08_NEW_PUB.seq: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2558	100.0	2811	15	US-10-324-985A-4
2	2558	100.0	2811	19	US-10-753-267-107
3	2402	93.9	1570	10	US-09-526-043-1
4	2402	93.9	1570	17	US-10-394-043-1
5	2105.5	82.3	2729	19	US-10-895-225A-36
6	2105.5	82.3	2978	10	US-09-955-999-43
7	2100.5	82.1	2626	18	US-10-324-985A-1
8	2100.5	82.1	2626	19	US-10-713-678-5
9	2100.5	82.1	2626	19	US-10-713-678-5
10	2100.5	82.1	2626	19	US-10-895-225A-56
11	2099.5	82.1	2181	14	US-10-072-036-70
12	2099.5	82.1	2184	14	US-10-072-036-138
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15	2099.5	82.1	2610	17	US-10-641-643-1206
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18	2099.5	82.1	2610	19	US-10-823-433-3
19	2004	78.3	1599	15	US-10-324-985A-3
20	2004	78.3	1599	15	US-10-641-643-1004
21	2004	78.3	1715	15	US-10-007-926A-354
22	2004	78.3	1715	19	US-10-735-461-23
23	2004	78.3	2562	18	US-10-322-281-415
24	1998	78.1	1722	18	US-10-322-281-412
25	1998	78.1	1741	15	US-10-324-985A-2
26	1998	78.1	1741	19	US-10-735-461-21
27	1998	78.1	3010	19	US-10-895-225A-57
28	1798.5	70.3	1254	18	US-10-713-678-3
29	1641.5	64.2	3712	18	US-10-473-939-7
30	1637	64.0	1140	15	US-10-324-985A-5
31	1511.5	59.1	1854	14	US-10-198-846-9984
32	1334	52.2	2410	9	US-09-771-161A-66
33	1236	48.3	879	17	US-10-424-599-21419
34	992	38.8	968	9	US-09-771-161A-65
35	960	37.5	758	9	US-09-910-943-677
36	949.5	37.1	1335	17	US-10-116-275-285
37	916	35.8	1338	16	US-10-067-977-1
38	916	35.8	1338	18	US-10-827-272-1
39	914.5	35.8	3196	17	US-10-094-749-222
40	913	35.7	1315	17	US-10-403-161-3
41	913	35.7	2343	17	US-10-403-161-1
42	913	35.7	2354	16	US-10-210-120-22
43	913	35.7	2365	9	US-09-981-353-6
44	909	35.5	2370	9	US-09-969-347-214
45	909	35.5	2370	9	US-09-880-107-3855

ALIGNMENTS

RESULT 1
US-10-324-985A-4
; Sequence 4, Application US/10324985A
; Publication No. US20030144204A1
; GENERAL INFORMATION:
; APPLICANT: Spencer, David
; TITLE OF INVENTION: Akt-based Inducible Survival Switch for Gene Therapy
; FILE REFERENCE: P02248US1/10106761
; CURRENT APPLICATION NUMBER: US/10/324,985A
; PRIOR FILING DATE: 2002-12-19
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 2811
; TYPE: DNA
; ORGANISM: human
US-10-324-985A-4

Alignment Scores:

Pred. No.: 6,866-280 Length: 2811
 Score: 2558.00 Matches: 479
 Percent Similarity: 100.00% Conservative: 0
 Beec Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 15 Gaps: 0

US-09-869-079B-3 (1-479) X US-10-324-985A-4 (1-2811)

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QY 21 AsnTrpArgProArgTrpPheLeuLeuLysThrAspGlySerPheIleGlyTrpLysGlu 40
DB 61 AACTGGAGGCCAGATACCTCTTTGAAAGACAGATGGCTCATTCATAGGATATATAAG 120
QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAspPheSerValAlaLysCysGln 60
DB 121 AAACCTCAAGATGTGATTTACTTATCCCTCAACACATTTTCAATGGCAAAATCCAG 180
QY 61 LeuMetLysThrGluArgProLysProAsnTrpPheIleIleArgCysLeuGlnTrpThr 80
DB 181 TTATATGAAAAACAGAACGACCAAGCCAAACACATTTATATACAGATGTCTCCAGTGCAGCT 240
QY 81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTrpThrGlu 100
DB 241 ACTGTTATAGAGAACATTTTCATGTAGATCTCCAGAGAAAGGAAAGATGACAGAA 300
QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGluGluGluLysArgMetAspCysSer 120
DB 301 GCTATCCAGGCTGTAGACAGACAGCTGCAGAGCAAGAGAGAGAGAGAAATGATTTGAG 360
QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrTrpHis 140
DB 361 CCAACTCTCAAAATTTATATATATAGAGAGAGAAAGATGATCCCTCTCAACCCATCAT 420
QY 141 LysArgLysThrMetAspAspPheAspTrpLeuLeuLeuGlyLysGlyTrpPheGly 160
DB 421 AAAAGAAAGCAATGATGATTTTGACTATTTGAACCTATAGATTAAGGCACCTTTGGG 480
QY 161 LysValIleLeuValArgGluLysValAspGlyLysTrpValMetLysIleLeuLys 180
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QY 181 LysGluValIleIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArgValLeu 200
DB 541 AAAAGAGTCATTTATTCAGAGATGAGATGGCACACACTCTAATAAGCAAGATATTA 600
QY 201 LysAsnTrpArgHisProPheLeuThrSerLeuLysTrpSerPheGlnTrpLysAspArg 220
DB 601 AAGAACATCTAGACATCCCTTTTAAACATCTCTGAATATTCCTCCAGACAAAGACCGT 660
QY 221 LeuCysPheValMetGluTrpValAsnGlyGlyGluLeuPhePheHisLeuSerArgGlu 240
DB 661 TTGTGTTTGTGATGGAATATGTTAATGGGGGAGAGCTGTTTTCATTTGTCGAGAGAG 720
QY 241 ArgValLysSerGluLysAspArgThrArgPheTrpGlyAlaGluIleValSerAlaLeuAsp 260
DB 721 CCGGTGTTCTCTGAGAGACCGCACACGTTTCTAAGGGGCAAAATTTCTCTGCTTGAG 780
QY 261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
DB 781 TATCTCATTTCCGAAAGATGTGTACCGTATCTCAAGTTGAGAGATCTTAATGCTGAGAC 840
QY 281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIleThrAspAla 300
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QY 301 AlaThrMetLysThrPheCysGlyThrProGluTrpLeuAlaProGluValLeuGluAsp 320
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QY 341 CysGlyArgLeuProPheTrpAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
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QY 361 GluAspIleLysPheProArgTrpThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
DB 1081 GAAGACATTAATTTCTCTGAAACACTCTCTTACAGATCAAAATCATTTGCTTACAGGGCTC 1140
QY 381 LeuIleLysAspProAsnLysArgLeuGlyGlyIleProAspAspAlaLysGluIleMet 400
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QY 401 ArgHisSerPhePheSerGlyValAsnTrpGlnAspValTyrAspLysLysLeuValPro 420
DB 1201 AGACACAGTTCTTCTCTGAGTAAACCTGCAAGATGATATGATTAATAAGCTTGACCT 1260
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DB 1261 CCTTTAAACCTCAAGTAAACATCTGAGACATCACTAGATTAATTTGATGAAGATTTTACA 1320
QY 441 AlaGlnThrIleThrIleThrProProGluLysTrpAspGluAspGlyMetAspCysMet 460
DB 1321 GCTCAGACTTATTCATTAACATTAACACACCTGAAATATATGATGAGATGCTATGAC 1380
QY 461 AspAsnGluArgArgProHisPheProGlnPheSerTrpSerAlaSerGlyArgGlu 479
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RESULT 2
US-10-753-267-107
; Sequence 107, Application US/10753267
; Publication No. US20050037946A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Stegiano, Nancy E.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Donoghue, Mary A.
; APPLICANT: Rodriguez-May, Amelie
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,
; TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,
; TITLE OF INVENTION: 9380, 2569654, 33566, 53656, 44143, 32612, 10671, 261,
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,
; TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,
; FILE REFERENCE: MP103-003P1RNM01M
; CURRENT APPLICATION NUMBER: US/10/753,267
; CURRENT FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 60/439,683
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/445,216
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,036
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/454,189
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/457,541
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/466,411
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/469,041
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/477,414

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; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/478,560
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/489,772
; PRIOR FILING DATE: 2003-07-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 2811
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1440)
US-10-753-267-107

Alignment Scores:
Pred. No.:      6,86e-280      length:      2811
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Query Match:    100.00%      Indels:      0
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US-09-869-079B-3 (1-479) x US-10-753-267-107 (1-2811)

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QY      21 AsnTPArProArgTrpPheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGlu 40
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QY      41 LysProGlnAspValAspLeuProGlyProLeuAsnAspPheSerValAlaLysCysGln 60
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QY      61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTrpThr 80
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QY      81 ThrValIleGluArgThrPheIleValAspThrProGluGluArgGluTrpThrGlu 100
DB      241 ACCTGATATAGAGAACATTTCAATGATATCTCCAGAGAAAGGGAAGATGACAGAA 300

QY      101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluGluArgMetLysSer 120
DB      301 GCTATCCAGGCTTTAGCAGACAGCTGCAAGGCGAAGAGAGAGAAATGAATGTAGT 360

QY      121 ProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrTrpHis 140
DB      361 CCAACTTCAAAATTTGATATATAGAGAGAGAAAGATGATGCTCTTCAACACCATCAT 420

QY      141 LysArgLysThrMetLysAspPheAspTyrLeuLysLeuGluGlyLysGlyThrPheGly 160
DB      421 AAAAGAAAGCAATGATGATTTTGACTATTTGAATTAAGTACTAGATTAAGGACCTTTGGG 480

QY      161 LysValIleLeuValArgGluLysAlaSerGlyLysTyrTrpAlaMetLysIleLeuLys 180
DB      481 AAAGTTATTTTGGTTGACAGAGAGGCAAGTGGAATAATCATGCTATAGAAATTCGAG 540

QY      181 LysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGlnSerArgValLeu 200
DB      541 AAAGAAGTCAATATTGCAAGAGATGAAGTGCAACACTTAAGTAAACAGAGATTA 600

QY      201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnTrpLysAspArg 220
DB      601 AAAGAACCTAGACATCCCTTTTAAACATCCCTTGAATAATTTCCCTCCAGAAAGACCGT 660

QY      221 LeuCysPheValMetGluTyrValLeuGlyGlyLeuPhePheHisLeuSerArgGlu 240

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QY      241 ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAlaLeuAsp 260
DB      721 CGGGTGTCTCTGAGGACCGCACACCTTTCTAATGAGGCAAGAAATTTCTCTGCTTGAC 780
QY      261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGluLysLeuMetLysAsp 280
DB      781 TATCTACATTCGGAAGAGATGTGTACCGGATCTCAAGTGTGAGAAATCTTAATGCTGGAC 840
QY      281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIleThrAspAla 300
DB      841 AAAGATGGCCACATAAATAATTAACAGATTTTGGACTTTGCAAAAGAGATCAAGATGCA 900
QY      301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeuGluAsp 320
DB      901 GCCACCATGAAAGCATTCGTGTGACATCCAGAAATATCTGACACAGAGGTGTTAAGAAAT 960
QY      321 AsnAspTyrGlyValArgAlaValAspTrpTrpGlyLeuGlyValValMetTyrGluMet 340
DB      961 AATGACTATGGCCGACAGAGACAGTGGTGGGCTTGAAGGCTGTCAATGTAAGAAATGATG 1020
QY      341 CysGlyValArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
DB      1021 TGTGGAGAGTTTACTTTCTTACAAACAGACAGACATGAAATCTTTGAAATTAATTAATG 1080
QY      361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
DB      1081 GAAGACATTAATTAATTTCTGCAACACTCTCTTCAGATGCAAAATCATTTGCTTCAAGGCTC 1140
QY      381 LeuIleLysAspProAsnLysArgLeuGlyGlyGlyProAspAspAlaLysGluIleMet 400
DB      1141 TTGATTAAGAGATCAATTAACGCTTGTGGAGGACAGATGATCAAAAGAAATTAATG 1200
QY      401 ArgHisSerPhePheSerGlyValAsnTrpGlnAspValTyrAspLysLysLeuValPro 420
DB      1201 AGACACAGTTTCTTCTCTGAGATTAACCTGCAAGATGTAATGATTAAGATTAATTAACCT 1260
QY      421 ProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGluLysPheThr 440
DB      1261 CTTTTAAACCTCAATTAACATCTGACAGACAGATCAATGATTTGATGAAAGATTTTACA 1320
QY      441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetLysAspMet 460
DB      1321 GCTCAACATTAATTAACATTAACACCACTGAAAAATATGAAGATGATGATGACCTGATG 1380
QY      461 AspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSerGlyArgGlu 479
DB      1381 GACAAATGAGAGGCGCGCATTTTCTCAATTTTCTTACTCTGCAAGTGGACAGAA 1437

RESULT 3
US-09-526-043-1
; Sequence 1, Application US/09526043
; Publication No. US20030100049A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagmont, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526,043
; EARLIER FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; NUMBER OF SEQ ID NOS: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

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LOCATION: (126) .. (1523)
US-09-526-043-1

Alignment Scores:

Pred. No.:	1,61e-262	Length:	1570
Score:	2402.00	Matches:	453
Percent Similarity:	98.91%	Conservative:	1
Best Local Similarity:	98.69%	Mismatches:	3
Query Match:	93.90%	Indels:	2
DB:	10	Gaps:	1

US-09-869-079B-3 (1-479) x US-09-526-043-1 (1-1570)

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QY 21 AsnTPArgProArgTyrPheIleuLeuIySerPheIleGlyTyrIyGlu 40
DB 186 AACTGAGGCGCAAGATACCTCTTTGAAGACAGATGGCTCATTCATGATATAAG 245
QY 41 LysProGlnAspValAspLeuProTyrProIleuAsnPheSerValAlaIysCysGln 60
DB 246 AAACCTCAAGATGTGATTTACCTTATCCCTCAACACTTTCAGTGGCAAAATGCCAG 305
QY 61 LeuMetIySerThrGluArgProIyProAsnThrPheIleIleArgCysLeuGlnTPThr 80
DB 306 TTTATGAAAACAGAACGACCAAGCAACATTTATATCATGATGTCTCCAGTGGACT 365
QY 81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTPThrGlu 100
DB 366 ACTGTTATAGAGAACATTTTCATGTAGATACCTCAGAGAAAGGAAAGATGACAGAA 425
QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGluGluGluArgMetAsnCysSer 120
DB 426 GCTATCAGAGCTGTACAGACAGACTGCAGAGCAAGAGAGAAATGAAATTTGTAGT 485
QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrHisHis 140
DB 486 CCAACTTCACAAATTATATATATATAGAGAGAGAAATGATGCTCTTCAACACCATCAT 545
QY 141 LysArgIySerThrMetAsnAspPheAspTyrLeuIyLeuLeuGlyIySerGlyTyrPheGly 160
DB 546 AAAAGAAACACATGATGATGATTTTGAATTTGAACTCTAGATGAAAGCACTTTTGG 605
QY 161 LysValIleIleuValArgGluIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 180
DB 606 AAAGTATTTTGGTGTGAGAGAGGCAAGTGAATACTATGCTATGAAAGATTTGAGAG 665
QY 181 LysGluValIleIleAlaIyAspGluValAlaHisThrIleuThrGluSerArgValIleu 200
DB 666 AAAGAAATCATTTATTCAGAAAGATGAGAGTGCACACACTTAACTAAAGCAGAGATTA 725
QY 201 LysAsnThrArgHisProPheIleuThrSerIleuIyIySerPheGlnThrIyAspArg 220
DB 726 AAGAACACTAGACATCTCTTTTAAACATCTTGAATAATTTCTCCAGCAAAAGACCT 785
QY 221 LeuCysPheValMetGluTyrValIaenGlyGluIleuPheHisIleuSerArgGlu 240
DB 786 TTGTGTTTGTGATGAAATATGTTAATGGGGGCACTGTTTTCATTTGTGAGAGAG 845
QY 241 ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAlaIleuAsp 260
DB 846 CGGGTCTTCTGAGAGACCGCACAGCTTTCTATGAGTGAAGAAATTTGCTGCTGGCAG 905
QY 261 TyrLeuHisSerGlyIyIyIleValTyrArgAspLeuIyIyIyIyIyIyIyIyIyIy 280
DB 906 TATCTCATATCCGGAAGATTTGTGACCGGATCTCAAGTTGAGAGATCTAATGCTGAG 965
QY 281 LysAspGlyHisIleIyIyIleThrAspPheGlyIyIyIyGluIyIyIyIyIyIyIy 300
DB 966 AAAGATGGCCACATAAATTTACAGATTTTGAATTTTGCAGAAAGAGGATCAACAGATGA 1025

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QY 301 AlaThrMetIySerPheCysGlyTyrProGluTyrLeuAlaProGluValIyIyIyAsp 320
DB 1026 GCCACCATGAAACATTTCTGTGCACTCCAGAAATATCTGGACACAGAGGTGTAGAGAT 1085
QY 321 AsnAspTyrGlyIyArgAlaValAspTPTrpGlyIyIyIyValIyIyMetIyIyIyMet 340
DB 1086 AATGACTAATGGCGAGCATGATCAGTGGGGCTTGAAGGGTGTGATGTATGAAATGATG 1145
QY 341 CysGlyIyArgLeuProPheTyrAsnGlnAspHisGlyIyIyIyLeuPheGluIleuMet 360
DB 1146 TTGGAGGTTACCTTTCTTACCAACAGACATGAGAACTTTTGAATTAATTAATG 1205
QY 361 GluAspIleIyPheProArgThrIleuSerSerAspAlaIySerIleuIyIyIyIyIy 380
DB 1206 GAAACATTAATTTCTTCCGAAACATCTTTCAGATGCAAAATCATTTGTTCAAGGGCTC 1265
QY 381 LeuIleIyAspProAsnIyArgLeuGlyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 400
DB 1266 TTGATTAAGATCCAAATTAAGCCTTGTGAGAGACAGATGATGCAAAAGAAATTAAG 1325
QY 401 ArgHisSerPhePheSerGlyValAsnTPGlnAspValTyrAspIyIyIyIyIyIyIy 420
DB 1326 AGACAGATTTCTTCTGTGAGTAACTGGCAAGATGATATGATTAATAAGCTTGTACT 1385
QY 421 ProPheIyProGlnValThrSerGluThrAspThrArgTyrPheAspGluIyIyIyIy 440
DB 1386 CTTTTTAAACCTCAAGTAACTCTGAGACAGATACATGATTTTGTATGAAGATTTACA 1445
QY 441 AlaGlnThrIleThrIleThrProProGluIyIyIyIyIyIyIyIyIyIyIyIyIyIy 459
DB 1446 GCTCAGACTATTAACATTAACACACCTGTAATAATGTCAAGCAATCA-----GATTTGT 1496

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RESULT 4

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US-10-394-568-1
; Sequence 1, Application US/10394568
; Publication No. US20040002136A1
; GENERAL INFORMATION:
; APPLICANT: GUN, KUN
; APPLICANT: IVASHCHENKO, YURI
; APPLICANT: CLARK, KENNETH L.
; TITLE OF INVENTION: INDUCTION OF VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
; FILE REFERENCE: A33990
; CURRENT APPLICATION NUMBER: US/10/394,568
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/584,938
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1570
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (126) .. (1523)
US-10-394-568-1

```

Alignment Scores:

Pred. No.:	1,61e-262	Length:	1570
Score:	2402.00	Matches:	453
Percent Similarity:	98.91%	Conservative:	1
Best Local Similarity:	98.69%	Mismatches:	3
Query Match:	93.90%	Indels:	2
DB:	17	Gaps:	1

US-09-869-079B-3 (1-479) x US-10-394-568-1 (1-1570)

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QY 1 MetSerAspValThrIleValIysGluGlyTPVAlGlnIleYserGlyGluIrrIleIys 20
DB 126 ATGAGCGATTACCACTTGTGGAAGAGGTGGTTCCAGAGGGGGAATATATATAA 185
QY 21 AsnTPArgProArgTyrPheIleuLeuIySerPheIleGlyTyrIyGlu 40

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Db 186 AACGGAGGCGCAAGATCTCTTGAAGACAGATGGCTCATTCATAGGATATTAAG 245
 Qy 41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheserValAlaLysCysGln 60
 Db 246 AAACCTCAAGATGGAGTTTAACTTATCCCTCAACAACTTTTCAGTGGCAAAATGCGAG 305
 Qy 61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnIleThr 80
 Db 306 TTAAATGAAACAGAACCAAGCCAAAGCCAAACATTATTAATCAGATCTCTCCAGTGGACT 365
 Qy 81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluIleThrPheGlu 100
 Db 366 ACTGTTATAGAGAAATTCATTGATGATCTCCAGAGAAAGGAAAGATGAGACGAA 425
 Qy 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCysSer 120
 Db 426 GCTATCCAGGCTGAGCAGACAGCTGCAAGGCGAAGAGAGAGAGAAATGAATTGATG 485
 Qy 121 ProThrSerGlnIleAspAsnIleGlyGluGluMetAspIleSerThrThrHis 140
 Db 486 CCAACTTCACAAATGTGATATATAGAGAGAGAGAGATGATGCTCTTACACCAATCAT 545
 Qy 141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuGluLysGlyThrPheGly 160
 Db 546 AAAAGAAAGACATGATGATTTGACTATTTGAAACTACTAGTTAAAGGCACTTTGGG 605
 Qy 161 LysValIleLeuValArgLysValAspGlyLysSerGlyLysTyrAlaMetLysIleLeu 180
 Db 606 AAAGTATATTTGGTTCAGAGAAAGGCAAGTGAATAATCATGCTATGAGATCTGAG 665
 Qy 181 LysGluValIleIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArgVal 200
 Db 666 AAAGAAAGTCAATATGCAAGAGATGAAGTGCACACACTGAACTGAAACCAAGATTTA 725
 Qy 201 LysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
 Db 726 AAGAACACTGACATCCCTTTTAACTCTTGAATAATCTCTCCAGCAAAAGACCT 785
 Qy 221 LeuCysPheValMetCysLysValAsnGlyGlyLeuLeuPhePheIleLeuSerArgGlu 240
 Db 786 TTGTGTTTGTGATGGAATGTGTTAATGGGGCGAGCTGTTTCCATTTGCGAGAGAG 845
 Qy 241 ArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAlaLeuAsp 260
 Db 846 CGGATGTTCTCTGAGAGCCGACACGCTTATGCGCAAAATGTCTGCTGCTGAGC 905
 Qy 261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
 Db 906 TATCTACATTCGCGAAAGATTTGTGACCGGATCTCAAGTTGAGAAATCTAATGCTGAGC 965
 Qy 281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIleThrAspAla 300
 Db 966 AAAGATGGCCACATAAAATTAACGATTTTGAACCTTGAAGAAGGATCACAGATGCA 1025
 Qy 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValIleLeuGluAsp 320
 Db 1026 GCCACCATGAAAGCATTTCTGCGACCTCCAGAAATATCTGACACAGAGGTTGAGAGAT 1085
 Qy 321 AsnAspTyrGlyArgAlaValAspTyrPheGlyLeuGluValAlaMetTyrGluMetMet 340
 Db 1086 AATGATCATGCGCGAGAGAGTGGATGGTGGGCTTACGAGGCTTGTATGAAATGATG 1145
 Qy 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGluLeuIleLeuMet 360
 Db 1146 TGTGGAGGTTTACTTTCTCAACACAGGACCATGAGAACTTTTGAATTAATTAATG 1205
 Qy 361 GluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeu 380
 Db 1206 GAAGACATTAATTTCTTCAGACATCTCTTCAGATGCAAAATCATTTGAGGAGCTC 1265
 Qy 381 LeuIleLysAspProAsnLysArgLeuGlyGlyProAspAspAlaLysGluIleMet 400

Db 1266 TTGATAAAGATCCAAATAAAGCCTTGGTGAGAGCCAGATGATGCAAAAGAAATTATG 1325
 Qy 401 ArgHisSerPhePheSerGlyValAsnTyrPheGlnAspValTyrAspLysLysLeuValPro 420
 Db 1326 AGACACAGATTTCTTCTCTGAGATMACTGGCAAGATGATATATATAAAAGCTTGATCCT 1385
 Qy 421 ProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
 Db 1386 CTTTTTAACCTCAAGTAAATCATCTGACACAGATCTAGATATTTTGTATGAAAGATTTACA 1445
 Qy 441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCys 459
 Db 1446 GCTCAGCATATTCAATTAACACACCTGAAAAATGTGACAGAAATCA-----GATTGT 1496
 RESULT 5
 US-10-895-225A-36
 ; Sequence 36, Application US/10895225A
 ; Publication No. US20050048587A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rao, Patricia
 ; APPLICANT: Snyder, Jessica
 ; APPLICANT: Bagley, Andria
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING TOLERANCE
 ; FILE REFERENCE: TUN-025
 ; CURRENT APPLICATION NUMBER: US/10/895,225A
 ; CURRENT FILING DATE: 2004-07-19
 ; PRIOR APPLICATION NUMBER: 60/488,502
 ; PRIOR FILING DATE: 2003-07-17
 ; NUMBER OF SEQ ID NOS: 161
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 36
 ; LENGTH: 2729
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-895-225A-36
 Alignment Scores:
 Pred. No.: 1,966-228 Length: 2729
 Score: 2105.50 Matches: 397
 Percent Similarity: 90.21% Conservative: 36
 Best Local Similarity: 82.71% Mismatches: 42
 Query Match: 82.31% Indels: 5
 DB: 19 Gaps: 4
 US-09-869-079B-3 (1-479) x US-10-895-225A-36 (1-2729)
 Qy 1 MetSerAspValThrIleValLysGluGlyTyrPheValGlnLysArgGlyGluTyrIleLys 20
 Db 276 ATAGCGAGCGTGGCTATTTGTGAAGAGGTTGGCTGCACAAACGAGGGAGTACATCAAG 335
 Qy 21 AsnTyrPheProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGlu 40
 Db 336 ACTGGCGGCGACAGCTACTTCCCTCCCAAGATGATGGACCTTATTTGGCTCAAGAGAG 395
 Qy 41 LysProGlnAspValAsp--LeuProTyrProLeuAsnAsnPheserValAlaLysCys 59
 Db 396 CGGCCCGCAGAGATGTGACCAACGTGAGGCTCCCTCCCAACAACTTCTCTGCGCGAGTGC 455
 Qy 60 GlnLeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnIleThr 79
 Db 456 CAGCTATGAAAGCGAGGCGGCCCGGCCCAACACCTTATCATTCCTGCTGCGCAGTGG 515
 Qy 80 ThrThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluIleThr 99
 Db 516 ACCACTGTATGAGAAAGCACTTCCATGATGAGACCTCTGAGGAGCGGAGAGTGGAGCA 575
 Qy 100 GluAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluGluArgMetAsnCys 119
 Db 576 ACCGCGCATCAAGCTGTGCTGCTGCAAGGCTCAAGAAACAGAGAGAGAGATGAGCTTC 635
 Qy 120 SerProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSerThrThrHis 139

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Db 636 CGGTCCGGCTCAACCCAGTGAACAATCAGGGCTGAAGAGATGAGGTGTCCCTGGCCAG 695
Qy 140 HisLys---ArgLysThrMetAsnAspPheAspTyrLeuLysLeuLysGlyThr 158
Db 696 CCCAAGACCCGGGTGACATGAACGATTGAGTACTGAAGTGTGTGGCAAGGGCACT 755
Qy 159 PheGlyLysValIleLeuValArgGlyLysAlaSerGlyLysTyrAlaMetLysIle 178
Db 756 TTCGGAGAGGTATCTCTGTGAAGGAGGACACAGGCGGCTACTACCCATGAAGATC 815
Qy 179 LeuLysLysGlyValIleIleAlaLysAspGlyValAlaHisThrLeuThrGluSerArg 198
Db 816 CTCAGAGAGGAAGTCACTCTGGCCAGAGCAGAGGTGGCCCACTCACTCCAGAGAACCC 875
Qy 199 ValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLys 218
Db 876 GTCTGCAAACTCCAGGCAACCCCTTCTCAACAGCCCTGAAGTACTCTTCCAGACCCAC 935
Qy 219 AsparGlyLeuCysePheValMetGlyTyrValAsnGlyGlyLysLeuPhePheHisLeuSer 238
Db 936 GACCGCTCTGCTTGTCTCATGAGTACGGCAACGGGGGAGGTGTCTTCCACCTGTCC 995
Qy 239 ArgGlyLysValPheSerGlyLysAspArgThrArgPheTyrGlyAlaGluIleValSerAla 258
Db 996 CGGAGCGGTGTCTCTCCAGAGCCGGGCGCTTCTATGGCGCTGAGATTGTGTCAAGCC 1055
Qy 259 LeuAspTyrLeuHisSerGlyLys---IleValTyrArgAspLeuLysLeuLysLeu 277
Db 1056 CTGGACTACTGCTGCTGAGAGAAAGCTGGTGTACCGGAGACTCAAGCTGGAGAACCTTC 1115
Qy 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCyseLysGlyLysIle 297
Db 1116 ATGCTGGAACAAGGACGGGACATTAAGTACAGACTTGGGGGTGTGCAAGAGGGGATC 1175
Qy 298 ThrAspAlaAlaThrMetLysThrPheCyseGlyThrProGluTyrLeuAlaProGluVal 317
Db 1176 AAGGACGGTCCACCAATGAAGACCTTTTCCGGCACCTGAGTACCTGGCCCCCGAGGTG 1235
Qy 318 LeuGluAspAsnAspTyrGlyArgAlaValAspTyrPheGlyLeuGlyValValMetTyr 337
Db 1236 CTGGAGACAATGACTACGAGCGCTGCAAGTGAAGTGTGGGGGCTGGGGCTGTGATGATAC 1295
Qy 338 GluMetMetCyseGlyArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGlyLeu 357
Db 1296 GAGATGATGTGGGTGCGCTGCGCTTCTAACAACAGACCATGAGAAAGCTTTTGTAGCTC 1355
Qy 358 IleLeuMetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377
Db 1356 ATCTCATGAGAGATGCGCTTCCGCGCACCGCTTGTCCCGAGGGCCAAAGTCTTGTCTT 1415
Qy 378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyLysProAspAspAlaLys 397
Db 1416 TCGGGGCTGTCAAGAGAGACCCCAAGCAGAGGCTGGGGGGCTCCGAGAGCGCAAG 1475
Qy 398 GluIleMetArgHisSerPhePheSerGlyValAsnTyrGlnAspValTyrArgLysLys 417
Db 1476 GAGATCATGACAGATGCTTCTTGTGCGGATATGTGTGGACAGCATGTACAGAGAAAG 1535
Qy 418 LeuValProProPheLysProGlnValThrSerGlnThrAspThrArgTyrPheAspGlu 437
Db 1536 CTCAGGCCACCTTCAAGGCCCGGAGTCAAGTCCGAGACTGACACCGGATTTTGTATGAG 1595
Qy 438 GluPheThrAlaGlnThrIleThrIleThrProGlnLysTyrArgGluAspGlyMet 457
Db 1596 GAGTTACGGCCCAAGATGATACCATCAACCACTGAGCCAA-----GATGACAGCAG 1649
Qy 458 AspCyMetAspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSerGly 477
Db 1650 GAGTGTGTGACACGAGGCGAGGCGCACTTCCCAAGTTCCTACTCGGCAAGCGG 1709
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RESULT 6
US-09-955-999-43
Sequence 43, Application US/09955999

```
Publication No. US20030036505A1
GENERAL INFORMATION:
APPLICANT: Barash et al.
TITLE OF INVENTION: Signal Transduction Pathway Component Polynucleotides, Polypeptide
TITLE OF INVENTION: Antidotes, and Methods Based Thereon
FILE REFERENCE: PT086P1
CURRENT APPLICATION NUMBER: US/09/955,999
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: 60/234,997
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 139
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43
LENGTH: 2978
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (28)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (2947)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (2973)
OTHER INFORMATION: n equals a,t,g, or c
US-09-955-999-43

Alignment Scores:
Pred. No.: 2,236-228 Length: 2978
Score: 2105.50 Matches: 397
Percent Similarity: 90.21% Conservative: 36
Best Local Similarity: 82.71% Mismatches: 42
Query Match: 82.31% Indels: 5
DB: Gaps: 4

US-09-869-079B-3 (1-479) x US-09-955-999-43 (1-2978)
Qy 1 MetSerAspValThrIleValLysGlyTyrValGlnLysArgGlyLysTyrIleLys 20
Db 491 ATGAGCGAGTGGCTATTTGTGAAGAGGTTGGCTGCACAAAGAGGAGTACATCAG 550
Qy 21 AsnTyrArgProArgTyrPheLeuLeuLysTyrAspGlySerPheIleGlyTyrLysGlu 40
Db 551 ACCGTGGCGGCAACGCTACTTCTCTCAAGATGATGAGCACTTATTGGTACAGAGG 610
Qy 41 LysProGlnAspValAsp---LeuProTyrProLeuAsnAsnPheSerValAlaLysCy 59
Db 611 CGGCGGAGAGTGTGACCAACGTAGAGGCTCCCTCAACACACTTCTGTGTGGCAGTGC 670
Qy 60 GluLeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCyseLysGlnTyr 79
Db 671 CAGCTGATGAAGAGAGGCGCCCGCCCAACACTTATATATCGCTGCTGCGAGTGG 730
Qy 80 ThrThrValIleGluArgThrPheHisValAspThrProGluLysArgGluLysTyrThr 99
Db 731 ACCACGTATGAAGACGACCTTCCATGTGAGACCTCGAGAGAGGGAGAGTGGACA 790
Qy 100 GluAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluLysArgMetLysCy 119
Db 791 ACCGCGATCCACACATGTGGCTACCGCCCTCAAGAGCAGAGAGAGAGATGAGCTTCC 850
Qy 120 SerProThrSerGlnIleAspAsnIleGlyGlyGluGluMetAspAlaSerThrThrHis 139
Db 851 CGGTGGGCTCAACCAAGTACCACTCAGGGGCTGAAGATGAGGTGTCTCCGTGGCCAG 910
Qy 140 HisLys---ArgLysThrMetAsnAspPheAspTyrLeuLysLeuLysGlyThr 158
Db 911 CCCAAGACCCGGGTGACATGAACGATTGAGTACTGAAGCTGTGGGCAAGGGCACT 970
Qy 159 PheGlyLysValIleLeuValArgGlyLysAlaSerGlyLysTyrTyrAlaMetLysIle 178
Db 971 TTCGGCAAGGTATCTGTGTGAAGAGAGGCGACAGGCGGCTACTACCCATGAAGATC 1030
```



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QY 278 MetLeuAspLysAspGlyHisIleYsIleThrAspPheGlyLeuCysIysGluGlyIle 297
    |||
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    |||
Db 1124 ATCTGGAAGAAGACCGGCAATCAAGATACGACTTGGGCTGTGCAAGAGGGGATC 1183
QY 298 ThrAspAlaAlaThrMetLysThrPheCysGlyThrProGluuTyLeuAlaProGluVal 317
    |||
    |||
    |||
Db 1184 AAGGATGTGGCCACTATGAAGACATTCGTGGGAACCCGAGTACTGGGCCCTGAGGTG 1243
QY 318 LeuGluAspAsnAspTyrGlyValAlaAspTyrTrpGlyLeuGlyValValMetCys 337
    |||
    |||
    |||
Db 1244 CTGGAGAGCAACACACTACGCGCTGTGAGACTGTGGGGCTGGGCGTGGTCAATGAT 1303
QY 338 GluMetMetCysGlyValArgLeuProPheTyrAsnGluAspHisGlyuLysLeuPheGluLeu 357
    |||
    |||
    |||
Db 1304 GAGATATGTGTGGCCGCTGCTGCTTCAACACAGACCAAGACGCTGTCGAGCTG 1363
QY 358 IleLeuMetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377
    |||
    |||
    |||
Db 1364 ATCTCATGTGAGAGATCCGCTTCCGCGCACACTCGGCCCTGAGGCCAAGTCCCTGCTC 1423
QY 378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyGlyProAspAspAlaLys 397
    |||
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    |||
Db 1424 TCCGGGCTGCTCAAGAGAGACCTTACACAGAGGCTGGTGGGCTCTGAAGATGCCAAG 1483
QY 398 GluIleMetArgHisSerPhePheSerGlyValAsnTrpGluAspValTyrAspLysLys 417
    |||
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    |||
Db 1484 GAGATATGTGACGACCGGCTTCTTGGCAACATGTGTGGCAGATGTGTGAGAGAGAG 1543
QY 418 LeuValProProPheLysProGluValThrSerGluThrAspThrArgTyrPheAspGlu 437
    |||
    |||
    |||
Db 1544 CTGAGGCCACCTTCAAGCCCGGCTGCTCACTGAGACAGACACAGTATTTCATGAG 1603
QY 438 GluPheThrAlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMet 457
    |||
    |||
    |||
Db 1604 GAGTTCACAGCTCAGATGATCACCATCACGCGCTGATCAA-----GATGACAGCATG 1657
QY 458 AspCysMetAspAsnGluArgArgProHisPheProGluPheSerTyrSerAlaSerGly 477
    |||
    |||
    |||
Db 1658 GAGTGTGTGACAGCTAGCGGAGGCGCGCACTTCCCAAGTTCCTACTACAGCATGGC 1717

RESULT 8
US-10-713-678-5
; Sequence 5, Application US/10713678
; Publication No. US20040122077A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/10/713,678
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/590,740
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2626
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-713-678-5

```

Alignment Scores:

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Pred. No.: 6,86e-228 Length: 2626
Score: 2100.50 Matches: 396
Percent Similarity: 90.00% Conservative: 36
Best Local Similarity: 82.50% Mismatches: 43
Query Match: 82.11% Indels: 5
DB: 18 Gaps: 4

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US-09-869-079B-3 (1-479) x US-10-713-678-5 (1-2626)

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QY 1 MetSerAspValThrIleValIysGluGlyTyrValGlnLysArgGlyGlyuTyTrpIleLys 20
    |||
    |||
    |||
Db 284 ATGAACGAGTGAAGCCATTCTGTGAAGAGGCGCTGGCAAAACGAGGGGAATATATTAA 343
QY 21 AsnTrpArgProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGlu 40
    |||
    |||
    |||
Db 344 ACCGTGGCGGCCAGCTACTTCTCTCTCAAGAACGATGGACCTTTATGTGCTACAGAGA 403
QY 41 LysProGluAspValAsp---LeuProTyrProLysAsnAspPheSerValAlaLysCys 59
    |||
    |||
    |||
Db 404 CGGCTTCAGATGTGATGATGACGAGAGATCCCACTCAACAACTTCTCAATGGCACATTC 463
QY 60 GlnLeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTrp 79
    |||
    |||
    |||
Db 464 CAGCTGATGAACAGAGGCGGCCAACGCCCAACCTTATCATCGCTGCTGAGGTG 523
QY 80 ThrThrValIleGluArgThrPheHisValAspThrProGluGluArgGlyuLysTrpThr 99
    |||
    |||
    |||
Db 524 ACCACAGTCATGAGGCGCACTTCCATGTGAAACGCTGAGAGGCGGGAAGAAATGGGCC 583
QY 100 GluAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetLysCys 119
    |||
    |||
    |||
Db 584 ACCGCCATTCAAGCTGTGGCCGATGAGACTCAAGAGCGAGAAAGAGACGATGACATTC 643
QY 120 SerProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSerThrThrHis 139
    |||
    |||
    |||
Db 644 CGATCAGGCTCACCCAGTGAACAATCAGGGGCTGAAGATGAGAGGTGCCCTGGCCAG 703
QY 140 HisLys--ArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyThr 158
    |||
    |||
    |||
Db 704 CCCAAGCACCGGTGTGCATGAGACGATGTGATGCTGAAACTGAGGCAAGGCGCACCC 763
QY 159 PheGlyLysValIleLeuValArgLysLysAsnGlyLysTyrTyrLysMetLysIle 178
    |||
    |||
    |||
Db 764 TTTGGAAAGTATTTCTGTGTAAGAGAGGACACAGCGCTGACTATGCTCAAGAGATC 823
QY 179 LeuLysLysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArg 198
    |||
    |||
    |||
Db 824 CTCAGAGAGAGATGATGTGCTCCCAAGATGAGTGGCCACAGCTTATCTAGAAACGT 883
QY 199 ValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLys 218
    |||
    |||
    |||
Db 884 GTCTGTCAGAACCTCAGGCACTCCCTTCTTACGCGCTCAAGTACTCATTCACAGCCAC 943
QY 219 AspArgLeuCysPheValMetGluTyrValAsnGlyGlyLeuPhePheHisLeuSer 238
    |||
    |||
    |||
Db 944 GACCGCTGTGCTTGTGATGAGATGACCAAGGGGAGACTCTTCTTCCACTGTCT 1003
QY 239 ArgGluArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAla 258
    |||
    |||
    |||
Db 1004 CGAGAGCGGCTGTCTCCGAGGACCGGCGCTTCTATGGTGGGAGATTGTGTCTGCC 1063
QY 259 LeuAspTyrLeuHisSerGlyLys--IleValTyrArgAspLeuLysLeuGluAsnLeu 277
    |||
    |||
    |||
Db 1064 CTGGACTACTTCCACTCCAGAGAAAGACGTGTGTACCGGAGACTGAGTGAAGAACTCC 1123
QY 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGlyIle 297
    |||
    |||
    |||
Db 1124 ATCTGGAAGAAGACCGGCAATCAAGATACGACTTGGGCTGTGCAAGAGGGGATC 1183
QY 298 ThrAspAlaAlaThrMetLysThrPheCysGlyThrProGluuTyLeuAlaProGluVal 317
    |||
    |||
    |||
Db 1184 AAGGATGTGGCCACTATGAAGACATTCGTGGGAACCCGAGTACTGGGCCCTGAGGTG 1243
QY 318 LeuGluAspAsnAspTyrGlyValAlaAspTyrTrpGlyLeuGlyValValMetCys 337
    |||
    |||
    |||
Db 1244 CTGGAGAGCAACACACTACGCGCTGTGAGACTGTGGGGCTGGGCGTGGTCAATGAT 1303
QY 338 GluMetMetCysGlyValArgLeuProPheTyrAsnGluAspHisGlyuLysLeuPheGluLeu 357
    |||
    |||
    |||
Db 1304 GAGATATGTGTGGCCGCTGCTGCTTCAACACAGACCAAGACGCTGTCGAGCTG 1363
QY 358 IleLeuMetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377

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Db 1604 GAGTTCACAGCTCAGATGATGATCAACATCAGCCGCTGATCAA-----GATGACAGCATG 1657

QY 458 AapCyMeAspAnsgluArgProHisPheProGlnPheSerTyrSerAlaSerGly 477

Db 1658 GAGTGTGTGACAGTGAAGGAGGCGCACTTCCCAAGTTCTTCACTCAGCAAGTGGC 1717

RESULT 10

US-10-895-225A-56

Sequence 56, Application US/10895225A

Publication No. US20050048587A1

GENERAL INFORMATION:

APPLICANT: Rao, Patricia

APPLICANT: Snyder, Jessica

APPLICANT: Bagley, Andria

TITLE OF INVENTION: METHODS FOR IDENTIFYING TOLERANCE

TITLE OF INVENTION: MODULATORY COMPOUNDS AND USES THEREFOR

FILE REFERENCE: TLN-025

CURRENT APPLICATION NUMBER: US/10/895,225A

CURRENT FILING DATE: 2004-07-19

PRIOR APPLICATION NUMBER: 60/488,502

PRIOR FILING DATE: 2003-07-17

NUMBER OF SEQ ID NOS: 161

SOFTWARE: PaateSeq for Windows Version 4.0

SEQ ID NO 56

LENGTH: 2626

TYPE: DNA

ORGANISM: Homo sapiens

US-10-895-225A-56

Alignment Scores:

Pred. No.: 6,86e-228 Length: 2626

Score: 2100.50 Matches: 396

Percent Similarity: 90.00% Conservative: 36

Best Local Similarity: 82.50% Mismatches: 43

Query Match: 82.11% Indels: 5

DB: 19 Gaps: 4

US-09-869-079B-3 (1-479) x US-10-895-225A-56 (1-2626)

QY 1 MetSerAspValThrIleValysGluGlyTrpValGlnIleAspArgGlyIleuTyrIleu 20

Db 284 ATGAGAGAGAGTACACATGTTGAAAGAGGCTGCTGCACAAAGAGGAGAAATATTATAA 343

QY 21 AsnTrpArgProArgTyrPheLeuLeuTyrAspGlySerPheIleGlyTyrIleuGlu 40

Db 344 ACCGTGGGCGGCAAGCTTCTCTCTCAAGAGATGGCACCTTTATGGCTTCAAGAA 403

QY 41 LysProGlnAspValAsp--LeuProTyrProLeuAsnAsnAspSerValAlaLysCys 59

Db 404 CGGCTCAGAGATGTGATCAGCAGAGAGTCCCACTCAACAACTTCACTGAGCAATGC 463

QY 60 GlnLeuMetLysThrGlnArgProLysProAsnThrPheIleIleArgCysLeuGlnTrp 79

Db 464 CAGCTATGAGAGCAGAGCGGCGCAAGGCCCAACACCTTTATCATCCGCTGCTGCAAGTGG 523

QY 80 ThrThrValIleGlnArgThrPheHisValAspThrProGlnGluArgGlnGluTrpThr 99

Db 524 ACCACAGTCAATTAGGGGCACTTCCATGTGAAACCGCTGAGAGGGGGAAGATGGGCC 583

QY 100 GlnAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGlnGluArgMetAsnCys 119

Db 584 ACCGCATTCAGACTGTGGCGGAGTCACTCAAGAGGAGGAGAAAGACGATGAGACTTC 643

QY 120 SerProThrSerGlnIleAspAsnIleGlyGlnGlnMetAspAlaSerThrTrpHis 139

Db 644 CGATCAGGCTCACCCAGTGAAGCTCAGGGGCTGAAGAGATGAGGTCTCCGCGCAAG 703

QY 140 HisLys--ArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyLys 158

Db 704 CCAAGACACCGCTGTGACCAATGAGAGAGTGTGAGTACTGAAATCTAGGGCAAGGGCAC 763

QY 159 PheGlyLysValIleLeuValArgGlyLysLeuSerGlyLysTyrTrpAlaMetLysIle 178

Db 764 TTTGGAAAGTATTTCTGTGAAAGAGAGGCCACAGCCGCTACTATGCAATGAGATC 823

QY 179 LeuLysLysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGlnSerArg 198

Db 824 CTCAGAAAGAGATCATGTCGCGCAAGATGAGTTGCCACACGCTTACTGAGAACCT 883

QY 199 ValLeuLysAsnThrArgHisAspPheLeuThrSerLeuLysTyrSerPheGlnThrLys 218

Db 884 GTCTGACAGACATCTAGAGCATCCCTTCCCTTACGGCCCTCAAGTACTCATTTCCAGACCAC 943

QY 219 AspArgLeuCysPheValMetGluTyrValAsnGlyGlyLeuLeuPheHisIleLeuSer 238

Db 944 GACCGCTCTGCTTTGTCAATGAGATGCAACCGGGGGGAGACTCTTCTTCCACCTGTCT 1003

QY 239 ArgGluArgValPheSerGluAspArgThrArgPheTyrGlyValGluIleValSerAla 258

Db 1004 CAGAGCGCGTGTCTTCCAGAGACCGAGCCCTCTTATGTGCGGAGATGTGTCTGCC 1063

QY 259 LeuAspTyrLeuHisSerGlyLys--IleValTyrArgAspLeuLysLeuGlnLeu 277

Db 1064 CTGACTACTTGCATCCGAGAAAGACGTGTGTACCGGAGCTGAAAGCTTGAGAACTTC 1123

QY 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGlyIle 297

Db 1124 ATGCTGAGACAGACCGGCGACATCAAGATACGAGACTTGGGCTGTGCAAGAGGGGATC 1183

QY 298 ThrAspAlaIleThrMetLysThrPheCysGlyThrProGlyTyrIleuAlaProGluVal 317

Db 1184 AAGATGTGTGCCATTTGAAAGACATTTCTGCGAAACCGCGAGTACTTGCCCTGAGGTG 1243

QY 318 LeuGluAspAsnAspTyrGlyValArgAlaValAspTrpTrpGlyLeuGlyValValMetTyr 337

Db 1244 CTGAGAGACAAAGACTACCGCGCTGCAAGTGTGAGCTGGTGGGGCTGTGATGAT 1303

QY 338 GlnMetMetCysGlyValArgLeuProPheTyrAsnGlnAspHisGlyLysLeuPheGlu 357

Db 1304 GAGATATGTGTGGCGCTGCTGCTTCAACACAGAGACCAAGAGAGTGTTCAGGCTG 1363

QY 358 IleLeuMetGluAspIleLysAspPheProArgTrpLeuSerSerAspAlaLysSerLeu 377

Db 1364 ATCTCATGAGAGAGATCCGCTTCCCGGCAACCTGCGCCCTGAGGCCAAGTCCCTGCTC 1423

QY 378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyGlyProAspAspAlaLys 397

Db 1424 TCCGGGCTGCTCAAGAGAGACCTTACAGAGAGGCTGAGGGGCTGTAGAGATGCGAAG 1483

QY 398 GlnIleMetArgHisSerPheSerGlyValAsnTrpGlnAspValTyrAspLysLys 417

Db 1484 GAGATCATCAGACCGGTTCTTGTTCACATCGTGTGACAGATGTATGAGAGAGAG 1543

QY 418 LeuValProProPheLysAspProGlnValThrSerGluThrAspThrArgTyrPheAspGlu 437

Db 1544 CTGAGCCCACTTTCAAGCCCAAGCTTCACTTGAAGTCAACCAAGATTTCCATGAG 1603

QY 438 GlnPheThrAlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMet 457

Db 1604 GAGTTCAGAGCTCAAGTATCAACATCAAGCCGCGCTGATCAA-----GATGACAGCATG 1657

QY 458 AapCyMeAspAnsgluArgProHisPheProGlnPheSerTyrSerAlaSerGly 477

Db 1658 GAGTGTGTGACAGTGAAGGAGGCGCACTTCCCAAGTTCTTCACTCAGCAAGTGGC 1717

RESULT 11

US-10-072-036-70

Sequence 70, Application US/10072036

Publication No. US20030082564A1

GENERAL INFORMATION:

APPLICANT: Ole THASTRUP

APPLICANT: Sara BURON

APPLICANT: Soren TULLIN

APPLICANT: Kasper ALMHOLT

APPLICANT: Kurt SCUDDER

TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An I


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/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: EGFP-PKB fusion
/ NAME/KEY: CDS
/ LOCATION: (1)..(2181)
US-10-072-036-138

Alignment Scores:
Pred. No.: 6,79e-228 Length: 2184
Score: 2099.50 Matches: 396
Percent Similarity: 90.19% Conservative: 36
Best Local Similarity: 82.67% Mismatches: 42
Query Match: 82.08% Indels: 5
DB: 14 Gaps: 4

US-09-869-079B-3 (1-479) X US-10-072-036-138 (1-2184)

QY 1 MetSerAspValThrIleValIysGluGlyTyrValGlnIleAspGlyGluTyrIleIys 20
DB 742 ATGAGCGACGTGGCTATGTGGAAGAGGGTGGCTGCACAAAGGAGGATACATCAAG 801
QY 21 AsnTPArgProArgTyrPheIleuLeuLysIleAspGlySerPheIleGlyTyrIleGlu 40
DB 802 ACCGCGCGGCGCACGCTACTTCCCTCCCAAGATGATGGCACCCTTCATGGCTACAGAGAG 861
QY 41 LysProGlnAspValAsp---LeuProTyrProLeuAsnAsnPheSerValAlaLysCys 59
DB 862 CGGCGCGAAGATGTGACCAACGTAGGCTCCCTCCCAACACTTCTCTGTGGCGCAGTGC 921
QY 60 GlnLeuMetLysThrGlnArgProLysProAsnThrPheIleIleArgCysLeuGlnTyr 79
DB 922 CAGCTGATGAAGCGAGGCGGCCCGGCCCAACACTTCATCATCCGCTGCGCGCAGTGC 981
QY 80 ThrThrValIleGlnArgThrPheIleValAspThrProGlnGluArgGluGluTyrThr 99
DB 982 ACCACGTGATCGAAGACGACCTTCATGTGAGACCTCTGAGAGGAGGAGGAGTGTGACA 1041
QY 100 GlnAlaIleGlnAlaValAlaAspArgLeuGlnGluGlnIleGluGluArgMetLysCys 119
DB 1042 ACCGCGCATCGACACTGTGGTGAAGCGGCTCCAGAACAGAGAGAGAGAGATGACATTC 1101
QY 120 SerProThrSerGlnIleAspAsnIleGlyGluGluGlnMetAspAlaSerThrThrHis 139
DB 1102 CGGTGGGGCTCACCCAGTGAACCTCAGAGGGCTGAAAGATGAGGTGTCCTCGGCCAAG 1161
QY 140 HisLys---ArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyThr 158
DB 1162 CCCAAGCACCGCGTGAACATGAACGAGTTGAGTACTGAAAGCTGCTGGGCAAGGCGACT 1221
QY 159 PheGlnLysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAlaMetLysIle 178
DB 1222 TTCGGCAAGGTATCTCGTGAAGAGAGAGCGCCAGCGCGCTACTACCGCATGAAGATC 1281
QY 179 LeuLysLysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGlnSerArg 198
DB 1282 CTCAGAGAGAGAGTCACTCGGCGCAAGAGAGAGTGGCCCACTACACCCAGAGACCGC 1341
QY 199 ValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLys 218
DB 1342 GTCCTGCAAACTCCAGGACCCCTTCCCTCAGCCCTGAAAGTACTCTTCCAGAGCCGAC 1401
QY 219 AspArgLeuCysPhePheValMetGluTyrValAsnGlyGluLeuPhePheHisLeuSer 238
DB 1402 GACCGCGCTGCTTGTTCATGAGTACGCCAACGGGGGCGAGGTGTTCCTCCACTGCTCC 1461
QY 239 ArgGluArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleValSerAla 258
DB 1462 CGGGAACGTGTGTTCTCCGAGGACCGGGGCGCGCTTCTATGAGCGCTGAGATTGTGAGCC 1521
QY 259 LeuAspTyrLeuHisSerGlyLys---IleValTyrArgAspLeuLysLeuGluAsnLeu 277
DB 277

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DB 1522 CTGACCTACCTGCACTCGGAGAGAAAGCTGTGTATCCGGGACCTCAAGCTGAGAACTTC 1581
QY 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIle 297
DB 1582 ATGCTGACAAAGAGCGGAGCACTTAAGATCAAGACTTCGGGCTGTGCAAGAGAGGGAGATC 1641
QY 298 ThrAspAlaIleThrMetLysThrPheCysGlyThrProGlnTyrLeuAlaProGluVal 317
DB 1642 AAGGACGGTGCACATGAAAGACTTTTGGCGCACACCTGAACTACCTGCCCCCGAGGTG 1701
QY 318 LeuGluAspAsnAspTyrGlyArgAlaValaAspTyrPheGlyLysGlyValValaMetTyr 337
DB 1702 CTGAGAGAAATGACTACGCGCGTGAAGAGCTGTGGGGGCTGGGCTGGGTCATGTAC 1761
QY 338 GluMetMetCysGlyArgLeuProPheTyrAsnGlnAspHisGlnLysLeuPheGluLeu 357
DB 1762 GAGATGATGTGGGTGCGCTGCGCTCTTCAACACAGAACATGAGAGCTTTTGAAGCTC 1821
QY 358 IleLeuMetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377
DB 1822 ATCTCATGAGAGATCCGCTTCCCGCGCACGCTTGTGCCGAGGCCMAAGTCTTGTCTT 1881
QY 378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyProAspAspAlaLys 397
DB 1882 TCAAGGCTGTCAAGAAAGACCCCAAGCAGAGGCTTGGGGGGCTCCGAGAGCCGCAAG 1941
QY 398 GlnIleMetArgHisSerPhePheSerGlyValaAsnTyrGlnAspValTyrAspLysLys 417
DB 1942 GAGATCATGACATTCGCTTCTTCCGCTATCGTGTGGCACAGCTGATGACAGAAAGAG 2001
QY 418 LeuValProProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGlu 437
DB 2002 CTCAGCGCCACCTTCAAGCCCGAGGTGACGTGAGAGACTGACACAGGATATTTGATGAG 2061
QY 438 GlnPheThrAlaGlnThrIleThrIleThrProProGlnLysTyrAspGluAspGlyMet 457
DB 2062 GAGTTCAAGCGCCCAAGATGATCAATCAACACCACTGAGCAAC-----GATGACAGCATG 2115
QY 458 AspCysMetAspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSer 476
DB 2116 GAGTGTGTGAGACAGAGAGCGGCGCCCACTTCCCGCAAGTTTCTACTCGGCCAGC 2172

RESULT 13
US-09-970-000-3
: Sequence 3, Application US/09970000
: Patent No. US20020127214A1
: GENERAL INFORMATION:
: APPLICANT: Hemmings, Brian Arthur
: TITLE OF INVENTION: Rac-Protein Kinase as Therapeutic Agent
: NUMBER OF SEQUENCES: 4
: OR In Diagnostics
: CORRESPONDENCE ADDRESS:
: ADDRESSER: No. US20020127214A1aIatis Patent and Trademark Department
: STREET: 564 Morris Avenue
: CITY: Summit
: STATE: NJ
: COUNTRY: USA
: ZIP: 07901-1027
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/970,000
: FILING DATE: 03-Oct-2001
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/068,702
: FILING DATE: 13-May-1998
: APPLICATION NUMBER: PCT/EP96/04810
: FILING DATE: 11-May-1996
: APPLICATION NUMBER: GB 9523379.7
: FILING DATE: 16-May-1995

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APPLICATION NUMBER: GB 9525704.4
 FILING DATE: 15-Dec-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Furman, Diane E.
 REGISTRATION NUMBER: 31,104
 REFERENCE/DOCKET NUMBER: 4-20635/A/PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 522-6924
 TELEFAX: (908) 522-6955
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2610 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: Human RAC alpha
 NAME/KEY: CDS
 LOCATION: 199..1641
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 199..1641
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-970-000-3

Alignment Scores:

Pred. No.:	8,846-228	Length:	2610
Score:	2099.50	Matches:	396
Percent Similarity:	90.19%	Conservative:	36
Best Local Similarity:	82.67%	Mismatches:	42
Query Match:	82.08%	Indels:	5
DB:	9	Gaps:	4

US-09-869-079b-3 (1-479) x US-09-970-000-3 (1-2610)

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QY      1 MetSerAspValThrIleValysGluGlyTTPValGlnLysArgGluGlyTyrIleLys  20
DB      199 ATGAGCGAGTGGCTTTGTGAGAGAGGTTGGCTGACAAAGAGGAGTACATCAG  258
QY      21 AsnTPArgProArgTyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGlu  40
DB      259 ACCTGGCGGCGACGCTACTTCCCTCCCAAGATGATGGGACCTTCAATTGGCTACAAAGAG  318
QY      41 LysProGlnAspValAsp--LeuProTyrProLeuAsnAsnPheSerValAlaLysCys  59
DB      319 CGGCCCGCAGAGTGTGACCAACGTCGAGGCTCCCTCAACAACTTCTGTGGCGCAGTGC  378
QY      60 GlnLeuMetLysThrGlnArgProLysProAsnThrPheIleIleArgCysLeuGlnTPR  79
DB      379 CAGCTATGAGAGCGGAGCGGCGCCCGCCCAACACCTTCACTCCGCTGCGCAGTGC  438
QY      80 ThrThrValIleGlnArgThrPheIleValAspThrProGlnGluArgGluGlnTPR  99
DB      439 ACCACGTGTCATGAAAGCACTTCCATGTGGAGACCTCTGAGAGGCGGAGGAGTGTGAC  498
QY      100 GlnAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluGluArgMetAsnCys  119
DB      499 ACCGCATCCAGACTGTGGTCGAGCGGCTTCACAAAGACAGAGGAGGAGGAGTGTGAC  558
QY      120 SerProThrSerGlnIleAspAsnIleGlyGluGlnLysAspAlaSerThrThrHis  139
DB      559 CGGTGGGCTCACCCGATGACATCTCAGGGGCTGAAAGATGGAGGTGTCTCCGCGCAAG  618
QY      140 HisLys--ArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyTyr  158
DB      619 CCCAAGCAGCGGCTGACATGAAAGAGTTGAGTACCTGAAGCTGTGGGCGAAGGCGACT  678

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QY      159 PheGlyLysValIleLeuValArgGluLysAlaSerGlyLysTyrTyrAlaMetLysIle  178
DB      679 TTGGCGAAGGTGATCTCGTGTGAGAGAGGACCAAGGCCGCTACTACCGCATGAAGATC  738
QY      179 LeuLysLysGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGlnSerArg  198
DB      739 CTCAAAGAGAAAGTATCTGTGGCAAGAGACGAGGTGGCCCACTACCTACCGAAGCCGC  798
QY      199 ValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLys  218
DB      799 GTCTCGCAAGACTCCAGGACCCCTTCTCCACAGGCTTCAAGTACTTCTCCAGACCCAC  858
QY      219 AspArgLeuCysPheValMetGluTyrValAlaGlnGlyLysLeuPhePheHisLeuSer  238
DB      859 GACCGCTCTGCTTGTCTATGAGAGTACGCCAACGGGGGGGAGCTGTCTTCCACCTGTCC  918
QY      239 ArgGluArgValPheSerGluAspArgThrArgPheTyrGlyValAlaGluIleValSerAla  258
DB      919 CCGGAACGTGTGTCTCCAGAGACCGGGCCGCTTCTATGGCGCTGAGTTGTGTACGCC  978
QY      259 LeuAspTyrLeuHisSerGlyLys--IleValTyrArgAspLeuLysLeuGluAsnLeu  277
DB      979 CTGACTACTGCTGACTCGGAGAAAGACGTGTGTACCGGACCTCAAGCTGGAGAACCTTC  1038
QY      278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuLysGluGlyIle  297
DB      1039 ATGCTGGAACAAGACCGGCACTTAAGATCACGACTGTGGCTGTGCAAGAGGGAGATC  1098
QY      298 ThrAspAlaAlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluVal  317
DB      1099 AAGGACGTCGCCACCATGAAGACCTTTCGGGACACCTGAGTACTGGCCCCCGAGGATC  1158
QY      318 LeuGluAspAsnAspTyrGlyValArgAlaValAspTPRTPRGLysGlyValValMetTyr  337
DB      1159 CTGAGAGCAAAATGACTACCGGCTGCACTGTGGTGGGGCTGGCTGGCTGACATGATC  1218
QY      338 GlnMetMetCysGlyValArgLeuProPheTyrAsnGlnAspHisGlnLysLeuPheGluLeu  357
DB      1219 GAGATGATGTGGCTGCTGCTGCTTCTTCAACACAGAGACCATGAGAGCTTTTGTAGCTC  1278
QY      358 IleLeuMetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu  377
DB      1279 ATCTCATGAGAGAGATCCGCTTCCCGGCAAGCTTGTGTCGAGGCCAAGTCTCTTGCT  1338
QY      378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyProAspAspAlaLys  397
DB      1339 TCAGGGGCTGCTCAAGAAAGACCCCAAGAGGCTTGGCGGGGCTCCGAGGACGCGCAAG  1398
QY      398 GlnIleMetArgHisSerPhePheSerGlyValAsnTPRGLAspValTyrAspLysLys  417
DB      1399 GAGATCATGACATCGCTTCTTTCGGGTATCGTGTGGCAGACGTTACGAGAGAGAG  1458
QY      418 LeuValProProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGlu  437
DB      1459 CTCAGGCCACCTTCAAGCCCAAGGTACGTGAGACATGACACACAGATTTTATGTAG  1518
QY      438 GluPheThrAlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMet  457
DB      1519 GAGTTCACGGCCCAAGATGATCATCATCACACCACTGACCAA-----GATGACAGCAG  1572
QY      458 AspCysMetAspAsnGluArgArgProHisPheProGlnPheSerTyrSerLeuAspSer  476
DB      1573 GAGTGTGTGACAGCGAGGCGAGGCCCACTTCCCAAGTTCCTACTGCGCCAGC  1629

```

RESULT 14

US-10-388-329
 ; Sequence 329, Application US/10388263
 ; Publication No. US20030228597A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cowser, Lex M.
 ; APPLICANT: Baker, Brenda F.
 ; APPLICANT: McNeill, John
 ; APPLICANT: Freier, Susan M.

APPLICANT: Sasmor, Henri M.
APPLICANT: Brooks, Douglas G.
APPLICANT: Ohashi, Cara
APPLICANT: Wyatt, Jacqueline R.
APPLICANT: Borchers, Alexander
APPLICANT: Vickers, Timothy A.
TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
MODULATION BY OLIGONUCLEOTIDES AND
TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
FILE REFERENCE: ISIS-4503
CURRENT APPLICATION NUMBER: US/10/388,263
CURRENT FILING DATE: 2003-03-12
NUMBER OF SEQ ID NOS: 947
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 329
LENGTH: 2610
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (199)...(1641)
US-10-388-263-329

Alignment Scores:
Pred. No.: 8,84e-228 Length: 2610
Score: 2099.50 Matches: 396
Percent Similarity: 90.19% Conservative: 36
Best Local Similarity: 82.67% Mismatches: 42
Query Match: 82.08% Indels: 5
DB: 17 Gaps: 4

US-09-869-079B-3 (1-479) x US-10-388-263-329 (1-2610)

QY 1 MetSeAspValThrIleValysGluGlyTyrPheValGluIleAspGluGlyTyrIleLeu 20
DB 199 ATGAGCGAGCTGCTATGTGGAGAGGTTGGCTCACAAAGAGGAGATCATCAAG 258
QY 21 AsnTyrArgProArgTyrPheLeuLeuIleThrAspGlySerPheIleGlyTyrIleVal 40
DB 259 ACCTGGCGGCGACGCTACTTCCCTCCCAAGATGAGGACCTTACTTGGCTTCAAGAG 318
QY 41 LysPheGlnAspValAsp--LeuProTyrProLeuAsnAsnPheSerValAlaLysCys 59
DB 319 CGGCCCGAGAGATGTGACCAACGTGAGGCTCCCTCAACACTTCTGTGGCGCAGTGC 378
QY 60 GlnLeuMetLysThrGlnArgProLysProAsnThrPheIleIleArgCysLeuGlnTyr 79
DB 379 CAGCTATGAGAGCGAGCGGCGCCGCGCCCAACACTTCACTCCGCTGCGCAGTGC 438
QY 80 ThrThrValIleGluArgThrPheIleValAspThrProGluGluArgGluTyrThr 99
DB 439 ACCACTGTATGAGAGCGACCTTCCATGTGAGACCTCTGAGAGGCGGAGAGATGAGAC 498
QY 100 GluAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluIleValLysCys 119
DB 499 ACCGCATCCAGACTGTGGCTGCGCTCAAGAACAGAGAGAGAGAGATGAGACTTC 558
QY 120 SerProThrSerGlnIleAspAsnIleGluGluGluMetAspAlaSerThrThrHis 139
DB 559 CGGTGGGCTCAACCGTGAACCTCAAGGGGCTGAAGAGATGAGGTGCTCTGGCCAA 618
QY 140 HisLys--ArgLysThrMetAsnAspPheAspTyrLeuLysLeuGluGlyLysGlyThr 158
DB 619 CCCAAGCAGCGCGTGAACGATGAGAGTGTGACTGACTGAGCTGCGGCAAGGCACT 678
QY 159 PheGlyLysValIleLeuValArgGluValAspSerGlyLysTyrTyrAlaMetLysIle 178
DB 679 TTCGGAGAGGTGATCTGTGAGAGAGAGGCGCAGCGCTACTACGCAAGAGATC 738
QY 179 LeuLysLysGluValIleIleAlaLysAspGluValAlaHisPheThrLeuThrGlnSerArg 198
DB 739 CTCAGAGAGAGATCATCTGTGCGCAAGAGAGAGATGAGGCTCCACACTCCGAGAACCGC 798

QY 199 ValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLys 218
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QY 219 AspArgLeuCysPheValMetGluTyrValaAsnGlyGlyLeuPhePheHisLeuSer 238
DB 859 GACCGCTCTGCTTGTCTATGAGTACCGCAACGGGGGGAGACTGTTCTTCCACCTGTC 918
QY 239 ArgGluArgValPheSerGlnAspArgThrArgPheTyrGlyValaGluIleValSerAla 258
DB 919 CCGAAGCTGTGTCTCCAGGAGCGGGCGCTTCTATGCGCTGAGATTGTTCAGCC 978
QY 259 LeuAspTyrLeuHisSerGlyLys--IleValTyrArgAspLeuLysLeuGluLeu 277
DB 979 CTGGAATACCTGCACTCGGAGAAAGACGTGTATCCGGGACTCAAGCTGAGAACTTC 1038
QY 278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIle 297
DB 1039 ATGCTGAGCAAGAGACGGGCACTTAAGATCACAGACTTCGGGCTGTGCAGAGAGGATC 1098
QY 298 ThrAspAlaIleThrMetLysThrPheCysGlyTyrProGluTyrLeuAlaProGluVal 317
DB 1099 AAGAGCGTGCACATGAGACCTTTTGGGCAACCTGAGTACTGCGCCCGAGGTG 1158
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QY 338 GluMetMetCysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeu 357
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QY 358 IleLeuMetGluAspIleLysPheProArgTyrThrLeuSerSerAspAlaLysSerLeuLeu 377
DB 1279 ATCTCATGAGAGATCCGCTTCCCGGACGCTTGTGCTCCGAGGCCAAGTCTTGTCT 1338
QY 378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyIleProAspAlaLys 397
DB 1339 TCAGGCGCTCTCAAGAGAGACCCCAAGAGAGCTTGGGGGGGCTCCGAGAGCGCAG 1398
QY 398 GluIleMetArgHisSerPheSerGlyValaAsnTyrGlnAspValTyrAspLysLys 417
DB 1399 GAGATCATGACACTGCTTCTTGTGCGGTATCGTGTGACACAGTGTACAGAGAAAG 1458
QY 418 LeuValProProPheLysProGlnValThrSerGluThrAspTyrArgTyrPheAspGlu 437
DB 1459 CTCAGCCCACTTCAAGCCCAAGCTGACGTGAGACTGACACCAAGTATTTTATGAG 1518
QY 438 GluPheThrAlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMet 457
DB 1519 GAGTTCAGCGCCCAAGTATGATCACTACACACCACTGACCA--GATGACAGCATG 1572
QY 458 AspCysMetAspAsnGluArgArgProHisPheProGlnPheSerTyrSerLysSer 476
DB 1573 GAGTGTGTGAGAGAGAGGAGGCGCCCACTTCCCAAGTCTCTTACTGCGCAGC 1629

RESULT 15
US-10-641-1206
Sequence 1206, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
Susan G. Stuart
Jeffrey J. Seilhamer
TITLE OF INVENTION: GENE EXPRESSION
COMPOSITION FOR THE DETECTION OF BLOOD CELL
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSES: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA

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      ZIP: 94304
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/10/641,643
      FILING DATE: 14-Aug-2003
      CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: <Unknown>
      FILING DATE: <Unknown>
      ATTORNEY/AGENT INFORMATION:
      NAME: Zeller, Karen J.
      REGISTRATION NUMBER: 37,071
      REFERENCE/DOCKET NUMBER: PA-0001 US
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (650) 855-0555
      TELEFAX: (650) 845-4166
      INFORMATION FOR SEQ ID NO: 1206:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 2610 base pairs
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      IMMEDIATE SOURCE:
      LIBRARY: GENBANK
      CLONE: g190827
      SEQUENCE DESCRIPTION: SEQ ID NO: 1206 :
US-10-641-643-1206

Alignment Scores:
      Pred. No.:      8.84e-228      Length:      2610
      Score:          2099.50         Matches:      396
      Percent Similarity: 90.1%       Conservative: 36
      Best Local Similarity: 82.67%   Mismatches:  42
      Query Match:      82.08%       Indels:       5
      DB:                17          Gaps:         4

US-09-869-079b-3 (1-479) x US-10-641-643-1206 (1-2610)
QY      1 MetSerAspValThrIleValLysGluGlyTrpValAlnLysAArgGlyGlyTrpIleLys 20
DB      199 ATAGAGCAGCTGCTATTTGAAAGAGGTTGGCTGCACAAACAGGGGAGTACATCAAG 258
QY      21 AsnTrpAArgProArgTrpPheLeuLeuLysThrAspGlySerPheIleGlyTrpLysGlu 40
DB      259 ACCTGGGGGCGCAGCTACTCTCTCTCAAGAAATGATGGCACCTTCATTGGCTACAGAG 318
QY      41 LysProGlnAspValAsp--LeuProTrpProLeuAsnAsnPheSerValAlaLysCys 59
DB      319 CGGCGCGAGATGTGGACCAACGTGAGGCTCCCTCAACAACCTTCTGTGGCGCAGTGC 378
QY      60 GlnLeuMetLysThrGluArgProLysProAsnThrPheIleIleLeuGlySerLeuGlnTrp 79
DB      379 CAGCTGATGAAGAGCGGCGGCGGCCCAACACCTTCATCACTCGCTCGCAGAGTGG 438
QY      80 ThrThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTrpThr 99
DB      439 ACCACGTGATCGAAGCGCACTTCGATGTGAGAGCTCTGAGAGCGGAGGAGAGTGACA 498
QY      100 GluAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluGluGluMetAsnCys 119
DB      499 ACCGCGCATCCAGCTGTGGCTGACGCGCTCAAGAGCAGAGGAGGAGAGAGTGAAGCTTC 558
QY      120 SerProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrThrHis 139
DB      559 CGGTGGGCTCAACCACTGACAGGAGCTGAAGAGATGGAGTGTCTCGGCCCAAG 618
QY      140 HisLys---ArgLysThrMetAsnAspPheAspTrpLeuLysLeuGluGlyLysGlyThr 158
DB      619 CCGAAGCAGCGCGTGAACATGAAGAGATTGAGTACTGAAGCTGTGGCGGCAAGGCACT 678

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QY      159 PheGlyLysValIleLeuValAArgGluLysAlaSerGlyLysTrpTrpAlaMetLysIle 178
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QY      179 LeuLysGluGluValIleIleAlaLysAspGluValAlaHisThrLeuThrGluSerArg 198
DB      739 CTCAAGAGAGATGATCTGTGGCCAGAGCAGAGTGGCCACACCTCACCGAGAACCCG 798
QY      199 ValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTrpSerPheGlnThrLys 218
DB      799 GTCCTGAGAACTCCAGGAGCACCCTTCTCTCAAGCCCTGAAGTACTCTTCCAGACCCAC 858
QY      219 AspArgLeuLysPheValMetGlyTrpValAsnGlyGlyGluLeuPhePheHisLeuSer 238
DB      859 GACCGGCTCTGCTTGTGATGAGTACGCCAACGGGGGCGAGGTGTTCTTCCACTGTGTC 918
QY      239 ArgGluArgValPheSerGluAspArgThrArgPheTrpGlyValAlaGluIleValSerAla 258
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QY      259 LeuAspTrpLeuHisSerGlyLys---IleValTrpArgAspLeuLysLeuGluAsnLeu 277
DB      979 CTGAGACTACTGCACTCGAGAGAGAACGTGGTGTACCGGAGCTCAAGCTGAGAACCTC 1038
QY      278 MetLeuAspLysAspGlyHisIleLysIleThrAspPheGlyLeuLysGlyGlyLys 297
DB      1039 ATGCTGACAAAGACGGGCGCATTAAGATCAAGACTTCGGGCTGTGCAAGAGGGGATC 1098
QY      298 ThrAspAlaIleThrMetLysThrPheCysGlyThrProGluTrpLeuAlaProGluVal 317
DB      1099 AAGAGCGGTGCCCACTGAAGACCTTTTGGGAGCACCTGAGTACTTGGCCCCCGAGGTG 1158
QY      318 LeuGluAspAsnAspTrpGlyArgAlaValAspTrpTrpGlyLeuGlyValAlaMetTrp 337
DB      1159 CTGAGAGACAAATGACTACAGCGCGTGCAGTGACTGGTGGGGGCTGGGCGGTGATGAC 1218
QY      338 GluMetMetCysGlyArgLeuProPheTrpAsnGlnAspHisGluLysLeuPheGluLeu 357
DB      1219 GAGATGATGTGCGGTGCGCTGCTCTTCAACACAGACCATGAGAGCTTTTGAAGCTC 1278
QY      358 IleLeuMetGluAspIleLysAspProAsnLysThrLeuSerSerAspAlaLysSerLeu 377
DB      1279 ATCTCATGAGAGAGATCCGCTTCCGCGCACCTTGTGTCGAGGCGAAGTCTTGTCTT 1338
QY      378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyGlyProAspAspAlaLys 397
DB      1339 TCAGGGCTGTCAAGAGAGACCCCAAGACAGAGGCTTGGGGGGGCTCCAGAGCGGCAAG 1398
QY      398 GluIleMetArgHisSerPhePheSerGlyValAsnTrpGlnAspValTrpAspLysLys 417
DB      1399 GAGATCATGAGCATGCTTCTTTCGCGGTATGTGTGGAGACGATGACGAGAGAGAG 1458
QY      418 LeuValProProPheLysProGluValThrSerGlnThrAspThrArgTrpPheAspGlu 437
DB      1459 CTCAGCCACCTTCAAGCCCAAGGTACGTCCGAGACTGACACAGATTTTATGAG 1518
QY      438 GluPheThrAlaGlnThrIleThrIleThrProGluLysTrpAspGluAspGlyMet 457
DB      1519 GAGTTCACCGGCCAAGATGATCAACATCACACCACTGACCAA-----GATGACAGCATG 1572
QY      458 AspCysMetCAspAsnGluArgArgProHisPheProGlnPheSerTrpSerAlaSer 476
DB      1573 GAGTGTGTGACGAGGAGGAGGCGGCCCACTTCCCAAGTTCCTTACTCGGCCAAG 1629

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Search completed: April 13, 2005, 11:52:56
 Job time : 719 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: April 13, 2005, 07:31:25 ; Search time 3598 Seconds
(without alignments)
5067.478 Million cell updates/sec

Title: US-09-869-079B-3

Perfect score: 2558

Sequence: 1 MSDVTVKSGWVQKRGSEYIK.....MDNRRPHRPFQSYSAAGRE 479

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=EST -OPMT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCH=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pco -NORH=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09869079.QCEN.1.1.5180.@runat.11042005.190024.13448 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELext=7

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est7: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2462	96.2	1445	3	BC020479 Homo sapi
2	2368	92.6	1440	3	AY393521 Homo sapi
3	2269	88.7	1394	9	AY393521 Mus muscu
4	1987	77.7	1829	3	AK040758 Mus muscu
5	1946.5	76.1	1829	3	BC068106 Mus muscu
6	1630	63.9	1440	9	AY393521 Pan trogl
7	1533	59.7	1136	1	AL545564 AL545564
8	1530.5	59.8	3724	3	AK028871 Mus muscu
9	1519	59.4	967	5	BU520318 AGNCOURT

10	1453.5	56.8	1015	1	AL548951
11	1449.5	56.7	1443	9	AY421689
12	1444.5	56.5	1443	9	AY421691
13	1442	56.4	1186	3	BC032709
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20	1347	52.7	1027	5	BQ062097
21	1338.5	52.3	1021	5	BQ944765
22	1325	51.8	776	7	CN526558
23	1322.5	51.7	999	7	BM559169
24	1320	51.6	760	7	CK639280
25	1316.5	51.5	860	5	BU552487
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27	1312.5	51.3	903	5	BU502645
28	1311.5	51.3	787	7	CK781668
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31	1304	51.0	1026	1	AL534146
32	1302.5	50.9	924	5	BU502654
33	1290.5	50.4	1082	6	CD502220
34	1289.5	50.4	858	7	CF551901
35	1287.5	50.3	942	5	BQ673953
36	1284.5	50.2	1053	5	BQ062455
37	1284	50.2	746	6	CB525973
38	1269	49.6	910	5	BQ880608
39	1267.5	49.6	936	5	BQ937145
40	1266	49.5	880	5	BU543038
41	1262.5	49.4	956	5	BQ919596
42	1252.5	49.0	903	5	BU197307
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45	1244	48.6	785	6	CA430499

ALIGNMENTS

RESULT 1	BC020479	1445 bp	mRNA	linear	HTC 19-NOV-2003
LOCUS	BC020479				
DEFINITION	Homo sapiens v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma), mRNA (CDNA clone IMAGE:3867931).				
ACCESSION	BC020479				
VERSION	BC020479.1	GI:18042842			
KEYWORDS	HTC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1445)				
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Sheman, C.M., Schlier, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, U., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usslin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loggellano, N.A., Peters, G.J., Adamson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Hale, S., Garcia, A.M., Gay, L.J., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Ruhl, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Shcherbina, Y., Sanchez, A., Whiting, M., Madan, A., Touchman, D.W., Green, E.D., Bouffard, G.G., Blakeley, R.W., Touchman, D.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E., Schneringer, A., Schein, J.E., Jones, S.J., and Marra, M.A.				

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE
22388257
PUBMED
12477932
REFERENCE
2 (bases 1 to 1445)
AUTHORS
Strausberg, R.
TITLE
Direct Submision
JOURNAL
Submitted (03-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing Center
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunnar, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louie, H.,
Kowals, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAX Plate: 13 Row: h Column: 23
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 19923313
This clone has the following problem: no polyA-tail.

FEATURES
source
Location/Qualifiers

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/cfeature_lib="NIH MGC_67"
/lab_host="DH10B"
/note="Vector: PCMV-SORT6"

ORIGIN

Alignment Scores:

Pred. No.: 5,24e-279 Length: 1445
Score: 2462.00 Matches: 461
Percent Similarity: 99.57% Conservative: 3
Best Local Similarity: 98.93% Mismatches: 2
Query Match: 96.25% Indels: 0
DB: 3 Gaps: 0

US-09-869-079b-3 (1-479) x BC020479 (1-1445)

QY 1 MetSerAspValThrIleValysGluGlyTTPValGlnIlyAspGlyGluTyrIleLys 20
DB 47 ATGAGCGATGTTACCTTGTGAAGAAGGTTGGGTCAGAGAAGGAGAAATATATAA 106
QY 21 AantPrArgProArgGyrPheLeuLeuLysThrAspGlySerPheIleGlyTyrLysGlu 40
DB 107 AACTGAGGCCAAGATTAATCTCTTGTGAAGACAGATGGCTCATTTAGATATAAAGAG 166
QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnPheserValAlaLysCysGln 60
DB 167 AAACCTCAAGATGTGAATTAATCTATCCCTCAACACATTTCACTGGCAAAATGCCAG 226
QY 61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTyrThr 80
DB 227 TTAAACAAAACAAGACAGACCAAGCAACACATTTATATATCAGATGTCTCCAGTGACT 286
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DB 287 ACTGTTATAGAGAACTTATCTATGTATGATCTCCAGAGGAAAGGAGATGAGACAGA 346

QY 101 AlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluArgMetAsnCysSer 120
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QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluMetAspAlaSerThrThrHis 140
DB 407 CCAACTTCACAATGATATATATAGAGAGGAGAGATGAGCCCTTCACAAACCCATCAT 466
QY 141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyThrPheGly 160
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DB 887 AAAGATGGCCACATATAAATTAACAGTTTGGACTTTGCAAGAGAGATCAAGATGCA 946
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QY 381 LeuIleLysAspProAsnLysArgLeuGlyGlyLysProAspAspAlaLysGluIleMet 400
DB 1187 TTGATTAAGATCCAAATTAACGCCCTTGGTGAAGACAGATGATGCAAAAGAAATTAATG 1246
QY 401 ArgHisSerPhePheSerGlyValAsnTyrGlnAspValTyrAspLysLeuValPro 420
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QY 421 ProPheLysProGlnValHisSerGluTyrAspThrArgTyrPheAspGluGluPheThr 440
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LOCUS   AY399351
DEFINITION Homo sapiens AKT3 gene, VIRTUAL TRANSCRIPT, partial sequence,
ACCESSION AY399351 1440 bp DNA linear GSS 15-DEC-2003
VERSION 1
KEYWORDS genomic survey sequence.
SOURCE  AY399351.1 GI:39755340
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferriere,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED  14671302
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferriere,S., Wang,G., Zheng,X.H., White,T.J., Sinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE   Direct Submision
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Alignment Scores:
Pred. No.: 6,46e-268 Length: 1440
Score: 2368.00 Matches: 450
Percent Similarity: 93.95% Conservative: 0
Best Local Similarity: 93.95% Mismatches: 29
Query Match: 92.57% Indels: 0
Gaps: 0
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Db 1 ATGAGGATGTTTACATGTGAAAGAGGTGGGTTTCAGAAAGGGAGAAATATATAAAA 60
QY 21 AsnTPArgProArgTyrPheLeuLeuIleYrAspGlySerPheIleGlyTyrIleGlu 40
Db 61 AACTGAGGCCAAGATTACTTCCTTTGAGACAGATGGCTCATTCATAGATATAAAGAG 120
QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAsnDheserValAlaIysCysGln 60
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QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrTrhHis 140
Db 361 CCACCTTCACAAATTATATATATAGAGAGAGAGAGATGATCCCTTACACCCATCAT 420
QY 141 LysArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyThrPheGly 160
Db 421 AAAAGAAAGCAATGATGATTTTGACTATTGAAACTAGCTAAGCACTTTTGGG 480
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QY 201 LysAsnThrArgHisAspPheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArg 220
Db 601 AAGAACACTAGACATCCCTTTTAAACATCCCTTGAATATTCCTCCAGACAAAGACCGT 660
QY 221 LeuCysPheValMetGluTyrValAlaGngIyGlyGluLeuPhePheHisLeuSerArgGlu 240
Db 661 TTGTGTTTGTGTATGAAATATGTTATGGGGGCGACGTGTTTCCATTTGTGAGAGAG 720
QY 241 ArgValPheSerGluAspArgTrpArgPheTyrGlyAlaGluIleValSerAlaLeuAsp 260
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QY 301 AlaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValIleGluAsp 320
Db 901 GCCACCATGAGACATTCGTGGCACTCCAGATATCTGGCACAGAGGTGTTAGAAAT 960
QY 321 AsnAspTyrGlyArgAlaValAspTrrPrrGlyLeuGlyValValMetTyrGluMetCec 340
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QY 341 CysGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMet 360
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Db 1141 TTGATTAAGGATCCAAATAAAGCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1200
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QY 421 ProPheLysProGlnValThrSerGluTrrAspThrArgTyrPheAspGluGluPheThr 440
Db 1261 CCTTTAAACCTCAAGTAACTATGAGACAGATCTAGATATTTTATATGAGAAATTTACA 1320
QY 441 AlaGlnThrIleThrIleThrProProGluLysTyrAspGluAspGlyMetAspCysMet 460
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LOCUS	AY399353	1394 bp	DNA linear GSS 15-DEC-2003
DEFINITION	Mus musculus AKT3 gene, VIRTUOL TRANSSCRIPT, partial sequence,		
ACCESSION	AY399353		
VERSION	AY399353.1		
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 1394) Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Ciavello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Slnsky,J.C., Adams,M.D. and Cargill,M. Interfing nonneutral evolution from human-chimp-mouse orthologous gene trios		
AUTHORS	Science 302 (5652), 1960-1963 (2003)		
JOURNAL	PUBMED		
REFERENCE	14671302		
TITLE	2 (bases 1 to 1394) Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tanenbaum,D.M., Ciavello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Slnsky,J.C., Adams,M.D. and Cargill,M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.		
COMMENT	Location/Qualifiers		
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Score:	2269.00	Matches:	432
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Best Local Similarity:	93.30%	Mismatch:	30
Query Match:	88.70%	Indels:	0
DB:	9	Gaps:	0
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Oy	37	glytyrlvlgsluylsproglnaspyvalaspleuprcotyrrproleuasnasnsheserval	56
Dd	63	GGCTTAAAGGAGAAAACCTCAAGATGTGACCTTACCCTCAACAACCTTCCAGTGTG	122
Oy	57	AlalyrCyBgInLemMerllyThrcJuvrgPrcOlysrProAsnthPhelIellayGvs	76
Dd	123	GAAAAATGTCAGTTAATGAAAAACAACAACCAAAAGCCAATAATTAATTCAGATGT	182
Oy	77	LengIntPrpThThValIlleglualvgrThrPhetSvalAspThProGlugluarglu	96
Dd	183	CTTAGCTGACCACTGTATATAGAGAACATTTCTATGATGATKACCCAGAGAAAGAGA	242
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Db	243	GAGTGAACGGAAGCTATCCAAAGCCGTCGACCGCATTTGCAGAGGCAAGAGGAGAGG	302
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Db	303	ATGAATTGTAGCCCAACCTTCACGATTGATTAATGTAGAGAAAGAGATGAGCGCTCT	362
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Db	363	ACAACCCCATCTAAAGAAAGAACAGATGAATATTGACTTATTTGAACCTATCGTAAGTAA	422
OY	157	GlyThrPheGlyValValIleLeuValArgGlyValysAlaSerGlyValysTyrTyrAlaMet	176
Db	423	GGCACTTTGGGAAGTATTATTTGCTTCGAGAGAAGCAAGTGGAAAATACTATGCTATG	482
OY	177	LysIleLeuValysGluValIleIleAlaLysAspGluValAlaHisPheLeuThrGlu	196
Db	483	AAGATTCGAAAGAAAGAAATCATATTATTCGAAAGGATGAGAGGACACACTTCATCGAA	542
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OY	237	LeuSerArgGluArgValPheSerGluAspArgThrArgPheTyrGlyAlaGluIleVal	256
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OY	257	SerAlaLeuAspTyrLeuHisAspGlyValGlyIleValIleTyrArgAspLeuLysLeuGluAsn	276
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Db	783	TTGATTCCTAGATTAAGATGATGCCATATATAAATTACGATTTTGGGCTTTGCAAGAAAGG	842
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Db	843	ATCACAGATGACGCTACCATGAAGACATTCGTGGCACACAGAGTACCTGGCACAGAG	902
OY	317	ValLeuGluAspAsnAspTyrGlyValArgAlaValAspTyrPheGlyLeuGlyValValMet	336
Db	903	GTATTAGAAAGTAAATGACTATGGCCGAGCCCTGACACTGTGGGCTTAAGGTGTGCTATG	962
OY	337	TyrGluMetMetCysGlyArgGluProPheTyrArgHisAspHisAspLysLeuPheGlu	356
Db	963	TATGAAATGATGTGTGGAAGGTTCCTTTCTACAAACGAGATCATGAGAACTCTTGAA	1022
OY	357	LeuIleLeuMetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeu	376
Db	1023	TTAATACTAAAGGAAGACATTAATTTCCCGGAACACTCTTCAGATGCAAAATCATTTG	1082
OY	377	LeuSerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyGlyProAspAspAla	396
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OY	457	MetAspCysMetAspAsnGluArgArgProHisPheProGluPheSerTyrSerAlaSer	476
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DEFINITION	AK040758	1848 bp	mRNA linear HTC 03-APR-2004
	Mus musculus adult male aorta and vein cDNA, RIKEN full-length		
	cDNA clone: A530023F15 product: thymoma viral		
ACCESSION	AK040758		
VERSION	AK040758.1	GI:26333954	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;		
AUTHORS	Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	Carninci, P., and Hayashizaki, Y.		
JOURNAL	High-efficiency full-length cDNA cloning		
MEDLINE	Meth. Enzymol. 303, 19-44 (1999)		
PUBMED	99279253		
REFERENCE	10349636		
AUTHORS	2		
TITLE	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		
JOURNAL	Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.		
MEDLINE	Normalization and subtraction of cap-trapper-selected cDNAs to		
PUBMED	prepare full-length cDNA libraries for rapid discovery of new genes		
REFERENCE	Genome Res. 10 (10), 1617-1630 (2000)		
AUTHORS	3		
TITLE	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,		
JOURNAL	Komno, H., Akiyama, J., Nishi, K., Kitenuki, T., Tashiro, H., Itoh, M.,		
MEDLINE	Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,		
PUBMED	Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiyagi, K.,		
REFERENCE	Fujiwara, S., Inoue, K., Togawa, Y., Izawa, Y., Ohara, E., Watanabe, M.,		
AUTHORS	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,		
TITLE	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.		
JOURNAL	RIKEN integrated sequence analysis (RISA) system--384-format		
MEDLINE	sequencing pipeline with 384 multicapillary sequencer		
PUBMED	Genome Res. 10 (11), 1757-1771 (2000)		
REFERENCE	4		
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the		
TITLE	FANTOM Consortium.		
JOURNAL	Functional annotation of a full-length mouse cDNA collection		
REFERENCE	Nature 409, 685-690 (2001)		
AUTHORS	5		
TITLE	The FANTOM Consortium and the RIKEN Genome Exploration Research		
JOURNAL	Group Phase I & II Team.		
REFERENCE	Analysis of the mouse transcriptome based on functional annotation		
AUTHORS	of 60,770 full-length cDNAs		
TITLE	Nature 420, 563-573 (2002)		
JOURNAL	6 (bases 1 to 1848)		
REFERENCE	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,		
AUTHORS	Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,		
TITLE	Hayashida, K., Hayatsu, N., Hizmoto, K., Hisoka, T., Hirozane, T.,		
JOURNAL	Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,		
MEDLINE	Kacoh, H., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Kouda, M.,		
PUBMED	Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,		
REFERENCE	Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohtsuo, N.,		
AUTHORS	Okazaki, Y., Saito, R., Saichou, H., Sasaki, K., Sasaki, K., Sakazume, N.,		
TITLE	Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,		
JOURNAL	Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,		
MEDLINE	Takeda, Y., Tanaka, T., Tomaru, A., Toy, T., Yasunishi, A.,		
PUBMED	Muramatsu, M., and Hayashizaki, Y.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (16-JUN-2001) Yoshinide Hayashizaki, The Institute of		
TITLE	Physical and Chemical Research (RIKEN), Laboratory for Genome		
JOURNAL	Exploration Research Group, RIKEN Genomic Sciences Center (GSC),		

COMMENT

Riken Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama
kanagawa 230-0045, Japan (E-mail: res@sc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9216)
Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

FEATURES

SOURCE

1. 1848
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mol_type="mRNA"
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ORIGIN

Alignment Scores:
Pred. No.: 8.65e-223 Length: 1848
Score: 1987.00 Matches: 384
Percent Similarity: 86.31% Conservative: 32
Best Local Similarity: 79.67% Mismatches: 42
Query Match: 77.68% Indels: 24
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US-09-869-079B-3 (1-479) x AK040758 (1-1848)

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Oy	41	LyeBProGlnApValasp---LeuProCYrrProleuaAnanPheserValAlalyCyS	59
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Db      657 TTTGGGAAGGATCTGTGTGAAGAGAGGACACAGCGCGCTACTATGCTCATGAAGATC 716
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Qy      219 AAPARGLeuCysePheValMetGlyTyrValAlaSerGlyGlyLysLeuPheHisLeuSer 238
Db      837 GACCCGCTGCTTGTCTCATGAGATGCGCAACGCGGCGGAGAGCTTCTTCCACCTGTCT 896
Qy      239 ArgGluArgValPheSerGluLysApeArgThrArgPheTyrGlyValAlaGluIleValSerAla 258
Db      897 CAGAGACGAGTGTCTTCCAGAGACCGGCGCCGCTTCTTATGATGCGGAGATGTGTGTC 956
Qy      259 LeuAspTyrLeuHisSerGlyLys---IleValTyrArgAspLeuLysLeuGluAenLeu 277
Db      957 CTGGACTACTTGTGACCTCCGAGAAAGACGGGTGTACTACGGGACCTGAGAGCTGAGAACCTTC 1016
Qy      278 MetLeuAspLysApeGlyHisIleLysValIleThrAspPheGlyLeuCyseLysGluGlyIle 297
Db      1017 ATGCTGGACAGAGACCGGCGACATCAAGATACCGACTTCGCGGTGTGCAAGAGGCGGATC 1076
Qy      298 ThrAspAlaIleThrMetLysThrPheCyseGlyThrProGluTyrLeuAlaProGluVal 317
Db      1077 AAGGACGGTCCCATATGAAAGACATCTGTGGAAACCCGAGATCCTGGGCCCTGTAGGATG 1136
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Qy      338 GluMetMetCyseGlyArgLeuProPheTyrAsnGlnAspHisGluLysLeuPheGluLeu 357
Db      1197 GAGATGATGTGTGGCGCGCTGCGCTTCTTCAACACAGGACCAACGAGAGCTGTTCCAGCTG 1256
Qy      358 IleLeuMetGluAspIleLysPheProArgThrLeuSerSerAspAlaLysSerLeuLeu 377
Db      1257 ATCTCTATGAGAGATCCGCTTCCGCGACACTCGGCCCTGAGGCCAAGTCCCTGCTC 1316
Qy      378 SerGlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyGlyProAspAspAlaLys 397
Db      1317 TCCGGGCTGCTCAAGAGAGCCTTACAGAGGCTCGTGGGGGCTCCAGAGATTCCAAAG 1376
Qy      398 GluIleMetArgHisSerPhePheSerGlyValAsnTyrGlnAspValTyrAspLysLys 417
Db      1377 GAGATCATCAGACACCGGCTTCTTGCACATCTGTGGCAGAGATGTGATGAGAAAG 1436
Qy      418 LeuValProProPheLysProGluValThrSerGluThrAspThrArgTyrPheAspGlu 437
Db      1437 CTGAGCCCACTTTCAGGCCCGGTCACCTCTGAGACTGACACCGAGTATTTCCATGAG 1496
Qy      438 Glu-PheThrAlaGlnThrIleThrIleThrProGluLysTyrAspGluAspLys 457
Db      1497 GAGTTTCAACAGCTCATATGATCATCAACGCGCGCTGAT----- 1536
Qy      457 CAspCyseMetAspAsnGluArgArgProHisPheProGln-PheSerTyrSerAlaSerG 477

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Db      1537 -----CAAATTCTCTACTGACGCAAGTG 1559
Qy      477 1y 477
Db      1560 GC 1561

RESULT 5
BC068106
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BC068106
Danio rerio cDNA clone IMAGE:6996896.
BC068106.1 GI:45751578
HTC.
Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 1829)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Burow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richard,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahy,J., Helton,E., Kettelman,M., Madan,A.C., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakeley,R.W., Touchman,A.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schultz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalun,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J., and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1829)
Strausberg,R.
Direct Submission
Submitted (24-MAR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Len Zou, Harvard
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth
Featherstone, Malachi Griffith, Odi Griffith, Ken Guin, Nancy Liao,
Kim Macdonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan North,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lilia Prabhu,
Parvaneh Saeedi, JR Santos, Angelique Scherch, Ursula Skalska,
Duane Smalun, Jeff Stott, Miranda Tsai, George Yang, Jacque
Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Series: IRAK Plate: 147 Row: b Column: 6
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, similarity but not identity to protein
This clone has the following problem: no cloning site /

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		/note="Vector: pExpressal"
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Percent Similarity:	86.164	Conservative: 49
Best Local Similarity:	76.034	Mismatches: 56
Query Match:	76.094	Indels: 11
DB:	3	Gaps: 5
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DB	153 ATGACGAGACTCACTGTTGTGTGAAGGAGGGCTGGCTCTTAAGAGAGGTGATCATCAAG	212
QY	21 AsnTPArgProArgTyrPheLeuLeuLythAspGlySerPheIleGlyTyrLyysGlu	40
DB	213 ACATGAGAGCCCGCGACTTCATCCCTGAGAGTACGCGCTCTTCATCGGCTACAGAG	272
QY	41 LysPProGlnAspValAspleuPro--TyrProLeuAsnAsnPheserValAlalyeCys	59
DB	273 AAGCCGAGCTACCGACGACGAGCTGTGACCCGCTCAACAACCTCTCTGTGGAGAGTGT	332
QY	60 GlnLeuMetLythThrGlnArgProLysProAsnThrPheIleIleArgCysleuGlnTyr	79
DB	333 CAGCTGATGAAACGAGGCGTCCGCGCGGACCACTTCATGATCCGCTGCTGCAGTGG	392
QY	80 ThrThrValIleGlnArgThrPheHisValAspThrProGlnGlnArgGlnGlnTyrThr	99
DB	393 ACCACCGTCATTTAGGGGACCTTCCTCATGTGACAGCATGACAGAGGAGCGAGTGTATG	452
QY	100 GlnAlaIleGlnAlaValAlaAspArgLeuGln--ArgGlnGlnGlnGlnArgMetAsn	118
DB	453 CGAGCAATCCAGATGGTGGCCCATGGGCTGCAGCGCGGGAGTGTGACGAGCCAGTGGAG	512
QY	119 CysSerProThrSerGlnIleAspAsnIleGlyGlnGlnGlnMetAspAlaSerThrThr	138
DB	513 ATCAAGTACAGCTCTCCACGATGCGCTGTGAGAGCATGAGATGTGTGTCCAATCC	572
QY	139 HisHisAlaYsArgLyserThrMetAsnAspPheAspTyrLeuLyseuLeuGlyLyysGlyThr	158
DB	573 ---ACGTCCAGAGTGCAGATGATGACTTTGATTACTTGAAGTGTGGGGGAAAGGCGACG	629
QY	159 PheGlyLyysValIleLeuValArgGlnLyAsaSerGlyLyserTyrTyrAlaMetCysIle	178
DB	630 TTGGGGAAGGTATTCTGTGGCGGAGAAAGGCTCTGGGATGTACTACGCAAGAGATC	669
QY	179 LeuLybLyysGlnValIleIleAlaLyAspGlnValAlaHisThrLeuThrGlnSerArg	198
DB	690 CTGGCCACAGGAGTGTATCTCGGAGAGGATGAAAGTGGCGCACACAGTCCACAGAGATCGA	749
QY	199 ValLeuLyAsnThrArgHisAspPheLeuThrSerLeuLyserTyrSerPheGlnThrIys	218
DB	750 GTTGTGCAAGACACTAGACCCCTTCCTTACCAAGCTTCAAAATACGCTTCCAGACTCAT	809
QY	219 AspArgLeuCysPheValMetGlnTyrValAsnGlyGlyGlnLeuPhePheHisLeuSer	238
DB	810 GACCGTCTGTGTTTCTGTATGAGATGACGCAAGGTGGAGAGCTATTCTTCCATCTGTCT	865
QY	239 ArgGlnArgValPheSerGlnAspArgThrArgPheTyrGlyValaGlnIleValSerAla	258

Db	870	CGTAGGGGTGTGTTCTCTGAGGATAGAGAGCTCGCTTACAGGGCGGTGAGATGTCGTCT	922
Oy	259	LeuApTyTrieuHissSerGlyLysIleValTyrArgAspLeuIleuGluAsnLeuMet	278
Db	930	CTGAGCTATATCTGCACCTACAGAGAGCGTGGTCTTACAGAGACCTGAAGCTGGAAACCTCATG	989
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Db	990	CTGATATATATGCGGACACATTTAAATACACAGACTTCGGTCTCTGTAAAGAGGATCA	1049
Oy	299	AspAlaIaIaThrMetLysThrPheCysGlyThrProGluTyrLeuAlaProGluValLeu	318
Db	1050	GACCAAGGCCACCATGAGAGACCTTCTGGCGGAGCCCAAGATATCTTGGCCCGGAGAGTCTGT	1109
Oy	319	GluAspAsnAspTyrGlyArgAlaValAspTyrTrpGlyLeuGlyValValMetTyrGlu	338
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Oy	339	MetMetCysGlyIleValGluLeuProPheTyrAsnGlnAspHisGlyLysIlePheGluLeuIle	358
Db	1170	ATGATGTGTGGCCCTCTGCGCTTCTTACAGTCACAGACACAGCGCTCTGTTGACAGATC	1229
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Oy	379	GlyLeuLeuIleLysAspProAsnLysArgLeuGlyGlyIleProAspAspAlaLysGlu	398
Db	1290	GGCTTCCTGAGGAAGAAGCCCAACACAGAGCTGGCGGAGGCCCAAGATGATGCCAGAGAT	1349
Oy	399	IleMetArgHisSerPhePheSerGlyValAsnTyrGlnAspValTyrAspLysLysLeu	418
Db	1350	GTCATGTATGCAACAGTTCTTCTCAGCGCGGTTCATGAGGACGATGTGCTGCAGAAAGCTG	1409
Oy	419	ValProProPheLysProGlnValThrSerGluThrAspThrArgTyrPheAspGluGlu	438
Db	1410	CTGCGCGCCCTTTAAACCGCAGGTACGTCAGAGACGAGACACGCTACTTGATGATGAG	1469
Oy	439	PheThrAlaGlnThrIleThrIleLeuThrProGluLysTyrAspGluAspGlyMetAsp	458
Db	1470	TTCACCTGCGCAGACATCATCTGTACCCCTCCAGACAG-----CTGAGC	1514
Oy	459	CysMetAspAsnGluArgArg-----ProHisPheProGlnPheSerTyrSerAla	475
Db	1515	TGTACAGACGCGAGAGAGTCTGGCGCATGCGACATTTCCCTCAGTTCTCTACTCGGCC	1574
Oy	476	SerGlyArgGlu 479	
Db	1575	AGCGTCCGAGAG 1586	
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DEFINITION	Pan troglodytes AKT3 gene, VIRTUAL TRANSCRIPT, partial sequence,		
ACCESSION	AY399352		
VERSION	AY399352.1	GI:39755341	
KEYWORDS	GSS.		
SOURCE	Pan troglodytes (chimpanzee)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.		
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,		
TITLE	Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,		
	Adams,M.D. and Cargill,M.		
	Inferring nonneutral evolution from human-chimp-mouse orthologous		
	gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PubMed	14671302		
REFERENCE	2 (bases 1 to 1440)		
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,		

Todd, M.A., Tanenbaum, D.M., Civejlo, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Satsky, J.T.,
Adams, M.D. and Cargill, M.

TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
Location/Qualifiers

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gene

ORIGIN

Alignment Scores:

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Best Local Similarity: 69.31% Mismatches: 147
Query Match: 63.72% Indels: 0
DB: 9 Gaps: 0

US-09-869-079B-3 (1-479) x AY39352 (1-1440)

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DB 1 ATGAGGAGATTACCAATTCGTAAGAGAGGTTGGCTCAGAGAGGAGAGATATATATAA 60
QY 21 AsnTPArgProArgTyrPheLeuLeuIysThsAspGlySerPheIleGlyTyrIleGlu 40
DB 61 AACTGAGGCCAGATACCTCTTTGAGACAGATGCTCATTCAATGATATATAAG 120
QY 41 LysProGlnAspValAspLeuProTyrProLeuAsnAspPheSerValAlaIysCysGln 60
DB 121 AAACCTCAAGATGGATTACCTTATCCCTCAACACTTTCAATGGCAAAATGCCAA 180
QY 61 LeuMetLysThrGluArgProLysProAsnThrPheIleIleArgCysLeuGlnTTPThr 80
DB 181 TTAATATAAACAAGACCAAGACCAAGCAACATTAATATAGATGCTCCAGTGACC 240
QY 81 ThrValIleGluArgThrPheHisValAspThrProGluGluArgGluGluTTPThrGlu 100
DB 241 ACGTTATAGAGACATTTCTATGATGATCTCCAGAGAAAGGAGAAATGACAGAA 300
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QY 121 ProThrSerGlnIleAspAsnIleGlyGluGluGluMetAspAlaSerThrTrpHisIle 140
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DB 721 NNN 780
QY 261 TyrLeuHisSerGlyLysIleValTyrArgAspLeuLysLeuGluAsnLeuMetLeuAsp 280
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QY 281 LysAspGlyHisIleLysIleThrAspPheGlyLeuCysLysGluGlyIleThrAspAla 300
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DB 1141 NNGATTAAGATCCAAATANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1200
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QY 421 ProPheLysProGluValThrSerGluThrAspThrArgTyrPheAspGluGluPheThr 440
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QY 461 AspAsnGluArgArgProHisPheProGlnPheSerTyrSerAlaSerGlyArgGlu 479
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RESULT 7
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LOCUS AL545564 Homo sapiens PLACENTA COR 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSOD1015YL1 5-PRIME, mRNA sequence.
ACCESSION AL545564
VERSION AL545564.3 GI:45746045
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1136)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:11267399.
CONTACT: Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7252.x

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?b=CSODI015CF060P1&c=7252.x.

FEATURES

source

Location/Qualifiers

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ORIGIN

Alignment Scores:

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Pred. No.: 1.59e-169 Length: 1136
Score: 1533.00 Matches: 301
Percent Similarity: 87.37% Conservative: 24
Best Local Similarity: 80.91% Mismatches: 43
Query Match: 59.93% Indels: 5
DB: 1 Gaps: 2

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US-09-869-079b-3 (1-479) x AL545564 (1-1136)

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QY 88 HisValAspThrProGluGluArgGluGluTTrpThrGluIleGlnIleValAlaAsp 107
DB 63 CATGTGAGACCTCTGAGAGCGGAGAGAGTGAACACCCCATCCAGACTGTGGTAC 122
QY 108 ArgLeuGlnArgGlnGluGluGluArgMetAsnCysSerProThrSerGlnIleAspAsn 127
DB 123 GGCCTCAAGAACGAGGAGGAGAGATGATGACTCCGGCGGGCTCACCAGCAAC 182
QY 128 IleGlyGluGluMetAspAlaSerThrHisIleLys--ArgLysThrMetAsn 146
DB 183 TCAGGGGCTGAAAGATGAGGTGCTCCCTGCCAACGCCCAAGACCCCGTGCATGAAAC 242
QY 147 AspPheAspTyrLeuLysLeuLysGlyLysGlyThrPheGlyLysValIleLeuValArg 166
DB 243 GAATTTGAGTACTGTAAGCTGCTGGGCAAGGCACTTTCGAGAGGTGATCTGTGTAAG 302
QY 167 GluLysLeuAspSerGlyLysTyrTyrAlaMetLysIleLeuLysGluValIleIleAla 186
DB 303 GAGAAAGCCACAGCGCGCTACTAGCCATGAAGTCTCTCAAGAAAGAAATCATCGTGGCC 362
QY 187 LysAspGluValAlaHisThrLeuThrGluSerArgValLeuLysAsnThrArgHisPro 206
DB 363 AAGAGAGAGGTGGCCACACACATCAGCAAGAACCGCTCTGCAAGAACTCCAGGACCC 422
QY 207 PheLeuThrSerLeuLysTyrSerPheGlnThrLysAspArgLeuCysPheValMetGlu 226
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QY 227 TyrValAsnGlyGluLeuPhePheHisLeuSerArgLysValArgValPheSerGluAsp 246
DB 483 TACGCCAACCGGGGCGAGCTGTTCTTCCACTGTCGCGGAAAGTGTTCTCCGAGAC 542
QY 247 ArgThrArgPheTyrGlyValGluIleValSerAlaLeuAspTyrLeuHisSerGlyLys 266
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DB 663 AAGATCAAGACTTCGGGGCTGTGCCAAGAGGGGATCAAGGACGGTCCACATGAAGACC 722
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QY 326 AlaValAspTyrTrpGlyLeuGlyValAlaMetTyrGluMetCysGlyArgLeuPro 345
DB 783 GCAGTGAAGCTGTGGGGGGCTGGCGGTGATCATTAAGATGATGTCGGGTCCCGCC 842
QY 346 PheTyrAsnGlnAspHisGluLysLeuPheGluLeuIleLeuMetGluAspIleLysPhe 365
DB 843 TTCTACAAACCAAGACCATGAGAAAGCTTTTGAAGCTCATCTTCATGAGAGATCCGCTTC 902
QY 366 ProArgThrLeuSer-SerAspAlaLysSerLeuLeuSerGlyLeuLeu-IleLysAsp 385
DB 903 CCGGCAAGCTGTGCTCCCGAGGCAAGTCTTGTTCAGGCTGCTCAAGAGAGACC 962
QY 385 roAsnLysArgLeuGlyGlyGlyProAspAspAlaLysGluIleMetArgHisSerPhe 405
DB 963 CCAAGCAGAGAGCTTGGCGGGGCTCCGAGAGAGCCAAAGAGATCATGACATCGCTTCT 1022
QY 405 heserGlyValAsnTrpGlnAspValTyrAspLysLysLeuValProProPheLysProG 425
DB 1023 TTCCCGGTATCGTGTGGSAGCMCGTGTACCAAAAAGCCAGACCCATTCAGACCCCM 1082
QY 425 InValThrSerGluThrAspThrArgTyrPhe 435
DB 1083 G-ATTMCGTGGGATGACCATGATATTT 1113

RESULT 8
AK028871
LOCUS
DEFINITION
MUS musculus 10 days neonate skin cDNA, RIKEN full-length enriched
library, clone:473245F20 product:thymoma viral proto-oncogene 2,
full insert sequence.
ACCESSION
AK028871
VERSION
AK028871.1 GI:26324815
KEYWORDS
HTC; CAP trapper.
SOURCE
MUS musculus (house mouse)
ORGANISM
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE
AUTHORS
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
METH. Enzymol. 303, 19-44 (1999)
PUBMED
99279253
10349636
2
REFERENCE
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Komoto, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Mitsuie, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)
PUBMED
20530913
JOURNAL
MEDLINE
20530913

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PUBMED 11076861
REFERENCE
AUTHORS
TITLE
JOURNAL
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JOURNAL
AUTHORS
COMMENT
FEATURES
source
CDS
ORIGIN
Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:

4
The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3724)
Aochi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hasegawa, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Yamamoto, M., and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://genome.gsc.riken.jp/
Location/Qualifiers
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KITDGLCKEGISDGAETKFTGCTPEYLALEEDNDGAVDMGGLGVNVMEMCG
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1. 85e-168 Length: 3724
1530.50 Matches: 285
89.86% Conservative: 34
Best Local Similarity: 80.28% Mismatches: 33

Query Match: 59.83% Indels: 3
DB: 3 Gaps: 2
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QY 145 MetAenAsPPhAsPTrLeuLySleuLengLyVysGlyThPhelLyysValIleLeu 164
DB 63 ATGAATGACTTGATTAATCTCAACCTCCGCAAGGAGCACTTCGCAAGTCACTTCG 122
QY 165 ValArgGlyLysAlaSerGlyLySryTrYrAlaMeLyIleLeuLySylGlyValIle 184
DB 123 GTTCGAGAGAGAGCCACTGCGCGCTATTATGCCATGAAATCTCGGCAAGAGTCAATC 182
QY 185 IleAlaLyAsPgluValAlaHsThrLeuThrGlySerArgValleuLySAsnThrArg 204
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QY 205 HsProPhelLeuThrSerLeuLySrySerPheGlnThLyAsPaArgLeuCySPhVal 224
DB 243 CACCCCTTCTTAAGAGCTCAAGTATGCTTCAGAGCCAGTACCGCTTATGCTTGTG 302
QY 225 MetGluTrValAsnGlyLyglUleuPhePheHsLeuSerArgGlyValPheSer 244
DB 303 ATGAGATGATCCACAGCGGGGTAGCTTTTCCACTCTCTCGGAGGAGTCTTCAGC 362
QY 245 GluAsPArgThrArgPheThyGlyAlaGluIleValSerAlaLeuAsPTrLeuHsSer 264
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QY 265 GlyLySleValTyArgAsPLeuLySleuGluAsnLeuMetLeuAsPTrLyS 284
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QY 285 IleLySleThAsPPhelLySleuCyLySylGlyIleThAsPAlaIaThrMeLyS 304
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QY 385 ProAsnLyArgLeuGlyLyglUlyProAsPAsPAlaLyglUleuMetArgHsSerPhe 404
DB 783 CCAAGACAGAGCTCGCGAGGCTCCAGTATGCGAAGAGAGTCTGAGCATATGATTC 842
QY 405 PheSerGlyValAsnTrpGlnAsPValTyAsPlyLySleuValProProPheLySPro 424
DB 843 TTCCTCAGATCACTGAGAGACGAGTGTGACAGAAAACCTCTGCGCACTTCAAACT 902
QY 425 GlnValThrSerGluThrAsPTrArgTyRpheAsPglUleuPheThrAlaGlnThrIle 444
DB 903 CAGGTCACTTCAAGATGACACAAAGTACTTGTATGACGAGTTCACCCCGAGTCCATC 962
QY 445 ThrIleThrProProGluTrLyArgPgluAsPgluMetAsPcyMetAsPAsnGluArg 464
DB 963 ACAATCAACACCCCAAGACCATATAT-----GACAGCTGTGACCCGCTGAACTGACACAG 1016

QY 465 ArgProHisPheProGlnPheSerTySerAlaSerGlyArgGlu 479
DB 1017 CGGACGCACTTCCCCAGTTCTCTACTCAGCCAGCATCCGAGAG 1061

RESULT 9
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LOCUS AGENCOURT 10157385 NIH_MGC_134 Mus musculus cDNA clone
DEFINITION IMAGE:6518260 5', mRNA sequence.
ACCESSION BUS20318
VERSION BUS20318.1 GI:22827844
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE NIH-MGC http://mgs.nci.nih.gov/
1 (bases 1 to 967)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@ds-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM14039 row: 1 column: 05
High quality sequence start: 16
High quality sequence stop: 729.

FEATURES
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1..967
Location/Qualifiers
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Cloned unidirectionally. Primer: Oligo dT. Average insert
size 1.7 kb. Constructed by Resgen, Invitrogen Corp. Note:
this is a NIH_MGC Library."

ORIGIN
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Score: 1519.00 Matches: 307
Percent Similarity: 97.16% Conservative: 1
Best Local Similarity: 96.85% Mismatches: 6
Query Match: 59.38% Indels: 6
DB: 5 Gaps: 0

US-09-869-079b-3 (1-479) x BUS20318 (1-967)

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DB 26 TTGGACTATTGAACTACTAGAGAA-GGCACCTTTGGGAAAGT-ATTGTTGTCGAGAG 83

QY 168 LysAlaSerGlyLeuTyrrAlaMetIleIleLeuLeuGlyGluValIleIleAlaLys 187
DB 84 AAGGCAAGTGGAAATACATGCTATGAAATCTCTGAAGAAAGATCATTTATGGCAAG 143

QY 188 AspGluValAlaHisThrLeuThrGluSerArgValLeuLysAsnThrArgHisProPhe 207
DB 144 GATGAAGTGGCAACACTCTTACTGAAAGCAGACTATAAGAACCAACACATTCATTT 203

QY 208 LeuThrSerLeuTyrrSerPheGlnThrLysAspArgLeuGlyPheValMetGlyTyr 227
DB 204 TTAACATCTTGAATATCTCTTCACAGACAAAGACCGTTGTGTTTGTGATGATATAT 263

QY 228 ValAsnGlyValGluLeuPhePheHisLeuSerArgGluArgValPheSerGluAspArg 247
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QY 248 ThrArgPheTyrrGlyValGluIleValIserAlaLeuAspTyrrLeuHisSerGlyLysIle 267
DB 324 ACAAGTTTCTATGATGTCAGAAATATGCTCTGCTTGAGACTATCTACATTCGGAAGATT 363

QY 268 ValTyrrArgAspLeuLeuGluGluAsnLeuMetLeuAspLysAspGlyHisIleLysIle 287
DB 384 GTGTACCGTGTATCTCAAGTTGGAGAAATTGATGCTGATGAAGATGCCATATAAAATT 443

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DB 444 ACCGATTTTGGGCTTTGCAAGAGAGATCAGATGAGCTTCCATGAAGACATTCCTGT 503

QY 308 GlyThrProGluLeuLeuAlaProGluValLeuGluAspAsnAspTyrrGlyArgAlaVal 327
DB 504 GGCACACCAAGATACCTGGGACAGAGTATTGAAGATATGATGATGCGGCGGCGTG 563

QY 328 AspTyrTrpGlyLeuGlyValValMetTyrrGluMetMetCysGlyArgLeuProPheTyr 347
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QY 348 AsnGluAspHisGluLeuLysLeuPheGluLeuIleLeuMetGluAspLysPheProArg 367
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QY 368 ThrLeuSerSerAspAlaLysSerLeuLeuSerGlyLeuLeuIleLysAspProAsnLys 387
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QY 388 ArgLeuGlyGlyGlyProAspAspAlaLysGluIleMetArgHisSer-PhePheSerGly 407
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QY 407 ValAlaAsnTrpGlnAspValTyrrAspLysLeuValProProPheLysProGlnValTh 427
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LOCUS AL548951 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1042YE16 5-PRIME, mRNA sequence.
ACCESSION AL548951
VERSION AL548951.3 GI:45749360
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1015)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polyes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 15, 2001 this sequence version replaced gi:31270773.
CONTACT: Genoscope
Genoscope - Centre National de Sequenage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a

[illegible]

US-09-869-079b-3 (1-479) x AY421691 (1-1443)

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 QY 41 LysPProGlnAspValAsp--LeuProTyrProLeuAsnAsnPheSerValAlaLysCys 59
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 Db 181 NNN 240
 QY 80 ThrThrValIleGlnArgThrPheHisValAspThrProGlnGluLysGluTyrPThr 99
 Db 241 NNN 300
 QY 100 GlnAlaIleGlnAlaValAlaAspArgLeuGlnArgGlnGluGluLysArgMetLysCys 119
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 QY 120 SerProThrSerGlnIleAspAsnIleGlyGluGlnMetAspAlaSerThrThrHis 139
 Db 361 CATCATGGCTCACCCAGTGAACCTAGAGGCGCTGAAGAGATGAGGTGTCCTCGGCCAAG 420
 QY 140 HisLys--ArgLysThrMetAsnAspPheAspTyrLeuLysLeuLeuGlyLysGlyThr 158
 Db 421 CCCAAGCACCGTGTGACCATGAACGAGTTGAGTACTGAGTACTGAGGCAAGGCAAC 480
 QY 159 PheGlyLysValIleLeuValArgGluValAspGlyLysTyrTyrAlaMetLysIle 178
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 QY 199 ValLeuLysAsnThrArgHisProPheLeuThrSerLeuLysTyrSerPheGlnThrLys 218
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 QY 219 AspArgLeuCysPheValMetGluTyrValAsnGlyGluLeuPheHisIleLysSer 238
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 Db 841 ATGCTGTGACAGAGACCGGACATCAAGATACCGACTTGGGGTGTGCAAGAGGGGAGATC 900
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 QY 398 GlnIleMetArgHisSerPhePheSerGlyValAsnTyrProlAspValTyrAspLysLys 417
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 Db 1321 GAGTTCACAGCTCAGATGATCATCATCAGCGCGCTGATCA-----GATGACAGCATG 1374
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RESULT 13
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 DEFINITION
 Homo sapiens, Similar to v-akt murine thymoma viral oncogene
 homolog 2, clone IMAGE:5496641, mRNA.
 ACCESSION
 BC032709
 VERSION
 BC032709.1 GI:21619713
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 HTG.
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE
 1 (bases 1 to 1186)
 Strausberg, R.
 Direct Submission
 Submitted (06-JUN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 CONTACT
 Contract: MGC help desk
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Lou Staudt
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mgc@nih.gov
 Akter, N., Ayle, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R.,
 Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stancirpop, S., Thomas, P.J., Touchman, J.W.,
 Teurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

FEATURES
 source
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 /organism="Homo sapiens"

Clone distribution: MGC clone distribution information can be found
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 Series: IRAK Plate: 69 Row: f Column: 14
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 6715585
 This clone has the following problem: frame shifted.


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Db      121  GTAGCCGACCGATTGCGAGAGCAAGAGAGAGATGATGTAGCCCAACCTCAG 180
QY      125  ILEASPASNILEGIUGIUGIUGIUMETASPAISERTHRHRHSISLYSARGLYSTHR 144
Db      181  ATTGATTAATTAAGAGAGAGAGATGATGCGCTTCAACCCATCATTAAGAGAGACG 240
QY      145  METASPAISERPHESPRTYRLEULYSLEULEUGIYLYSGIYTHRPHEGIYLYSVALILE 164
Db      241  ATGAATGATTTTGAATTAATTTGAACCTAGTAAAGGCACTTTGGAAAGTTATTTTG 300
QY      165  VALARGIULYSALASERGIYLYSTYRVALAMECLYSILEULEYSLYSGIULVALILE 184
Db      301  GYTCCGAGAGAGAGCAAGTGAATAATCTATGCTATGAAAGATTCGAAGAAAGATCAT 360
QY      185  ILEAIALYSAPGILUVALAIAHSITHRLEUTHRGLUSERARGVALLEULYSANTRARG 204
Db      361  ATTGCAAAAGATGATGAGGCAACACTCTTACTGAAGACAGACTTAAGAAACCCAGA 420
QY      205  HISPROPHLEUTHRSEULEULYSYRSERPHEGINTHRYSAPARGLEUCYSPHEVAL 224
Db      421  CATCCATTTTAAATCTTGAATATATCTTCCAGACAAAGACCGTTGTGTTTTGTG 480
QY      225  METGLUTYRVALANGIYGIYGIULLEUPHEPHEHISLEUSERARGIULARGVALPHE 244
Db      481  ATGGAATATGTTAATGCGGAGAGAGCTGTTTTCATTGTTCGAGAGAGCGAGTGTCT 540
QY      245  GLUASPARGTHRARGPHETYRGIYVALAGIUILEVALSERALALEUASPRTYRLEUHS 264
Db      541  GAGGACCGCACACGCTTCTATGAGGCAAAATGTCTCTGCTTGGACTATCTACATCT 600
QY      265  GILYLYSILEVALTYRARGAPLEULYSLEUGIUAASMEULEUPLYSASPGLYHS 284
Db      601  CGAAAGATTGTGTACCGTGATCTCAAGTTGAGAAATTTGATGCTAGATAAGATGGCAT 660
QY      285  ILEYSILETHRASPHEGIYLYSEUCYSLYSGIUGIYILETHRASPALAALATHRMET 304
Db      661  AATAAATTAACGATTTTGGCTTTGCAANAGAGGATCACAGATGCACCTACCATGAAG 720
QY      305  THRPHCYSGIYTHRPROGIUTYRLEUALAProGIUVALLEUGIUAASPAASPTYRGI 324
Db      721  ACATTCTGTGGCAACCAAGATACCTGGCACCAAGGATTTAGACGATTAATGACTATGG 780
QY      325  ARGALAVALASPRTPTPGIYLEUGIYVALIEMETYSR 337
Db      781  CGAGCCGTGGACTGTGGGCTTANGTGTGTATGAT 819
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